

## SEQUENCE LISTING

<110> Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A

<120> CHIMPANZEE ADENOVIRUS VACCINE CARRIERS

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<151> 2004-01-23

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&lt;210&gt; 6

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 20 Fiber

&lt;400&gt; 6

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atgaagcgca ccaaaacgtc tgacgagagc ttcaaccccg tgtaacccta tgacacggaa 60
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gatgccacag taagcactta ctccatgtca ttctcatgga actggaatgg aagtaattac 1680  
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<210> 7

<211> 1278

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 4 Fiber

<400> 7

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 gagaagcccc tgggggtggt gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180  
 gaaatcacc tcaagctggg agaggggggtg gacctcgatt cctcgggaaa actcatctcc 240  
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 aatatactga gaacaagcat tctaaacaca ctagcttttag gttttggatc aggttttaga 420  
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 aacataagct gggctaaagg tttaaaattt gaagatggag ccatagcaac caacattgga 600  
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 tacatcgccc aagaatga 1278

<210> 8

<211> 1335

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 5 Fiber

<400> 8

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 gagaagcccc tgggggtggt gtccctgcgt ctggccgacc ccgtcaccac caagaacggg 180  
 gaaatcacc tcaagctggg agatgggggtg gacctcgacc actcgggaaa actcatctcc 240  
 aacacggcca ccaaggccgc cgcccctctc agtttttcca acaacaccat ttcccttaac 300  
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 aagatattag acacagatct actaaaaaca cttgttgttg cttatgggca gggattagga 420  
 acaaacacca atggtgctct tgttgcccaa ctagcatacc cacttgtttt taataccgct 480  
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 attaattgca aaagaggtat ctatgtcact accacaaaag atgcactgga gattaatatc 600  
 agttgggcaa atgctatgac atttatagga aatgccattg gtgtcaatat tgacacaaaa 660  
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 caagtaaaac ttggagctgg tcttacattt gacagcacag gtgccattgt tgcttggaa 780  
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atcactttca atgaaactga tgatgaaacc tgtgattact gcatcaactt tcaatggaaa 1260
tggggagctg atcaatataa ggataagaca ctgcgaacca gttcattcac cttctcatac 1320
atcgcccaag aataa 1335

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&lt;210&gt; 9

&lt;211&gt; 1338

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 7 Fiber

&lt;400&gt; 9

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gagaagcccc tgggggtggt gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcacc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
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acaaacacca ctggtgccct tgttgcccaa ctagcagccc cacttgcttt tgatagcaat 480
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tacattgccc aagaatga 1338

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&lt;210&gt; 10

&lt;211&gt; 1278

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 9 Fiber

&lt;400&gt; 10

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atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtggt gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcacc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
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tacatcgccc aagaatga                                     1278

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&lt;210&gt; 11

&lt;211&gt; 1278

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 10 Fiber

&lt;400&gt; 11

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atgtccaaaa agcggtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
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gagaagcccc tgggggtgct gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcacc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
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&lt;210&gt; 12

&lt;211&gt; 1737

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 11 Fiber

&lt;400&gt; 12

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&lt;210&gt; 13

&lt;211&gt; 1632

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 16 Fiber

&lt;400&gt; 13

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aatgaatcca gtgaaactag ccaggtgagt cactactcca tgtcatttac gtgggcttgg 1560
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gctgaacaat aa

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<210> 14  
 <211> 1632  
 <212> DNA  
 <213> Chimpanzee Adenovirus-ChAd 17 Fiber

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 <212> DNA  
 <213> Chimpanzee Adenovirus- ChAd 19 Fiber

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&lt;210&gt; 16

&lt;211&gt; 2865

&lt;212&gt; DNA

&lt;213&gt; Chimp0anzee Adenovirus- ChAd 20 Hexon

&lt;400&gt; 16

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&lt;210&gt; 17

&lt;211&gt; 2823

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 4 Hexon

&lt;400&gt; 17

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<211> 2823

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 5 Hexon

<400> 18

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taa 2823

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&lt;210&gt; 19

&lt;211&gt; 2823

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 7 Hexon

&lt;400&gt; 19

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<210> 20

<211> 2793

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 9 Hexon

<400> 20

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&lt;210&gt; 21

&lt;211&gt; 2793

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 10 Hexon

&lt;400&gt; 21

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&lt;210&gt; 22

&lt;211&gt; 2883

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 11 Hexon

&lt;400&gt; 22

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a a c t a c a a c a	t c g g c t a c c a	g g g c t t c t a c	a t c c c a g a g a	g c t a c a a g g a	c a g g a t g t a c	2400
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g c c c c c a c c a	t g c g c g a g g g	a c a g g c c t a c	c c c g c c a a c t	t c c c c t a c c c	g c t c a t a g g c	2580
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c g c g g c g t c a	t c g a g a c c g t	g t a c c t g c g c	a c g c c c t t c t	c g g c c g g c a a	c g c c a c c a c c	2880
t a a						2883

&lt;210&gt; 23

&lt;211&gt; 2835

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 16 Hexon

&lt;400&gt; 23

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c t g g g g a a c a	a g t t t a g g a a	c c c c a c g g t g	g c g c c c a c g c	a c g a t g t g a c	c a c c g a c c g c	180
a g c c a g c g g c	t g a c g c t g c g	c t t c g t g c c c	g t g g a c c g c g	a g g a c a a c a c	c t a c t c g t a c	240
a a a g t g c g t	a c a c g c t g g c	c g t g g g c g a c	a a c c g c g t g c	t g g a c a t g g c	c a g c a c c t a c	300
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t a c a a c a g c c	t g g c c c c a a	g g g a g c t c c c	a a t t c c a g t c	a g t g g g a g c a	g a c g g a g a a c	420
g g g g g c g g a c	a g g c t a c g a c	t a a a a c a c a c	a c c t a t g g a g	t t g c c c c a a t	g g g t g g a a c t	480
a a t a t t a c a g	t c g a c g g a c t	a c a a a t t g g a	a c t g a c g c t a	c a g c t g a t a c	g g a a a a a c c a	540
a t t t a t g c t g	a t a a a a c a t t	c c a a c c t g a g	c c t c a g a t a g	g a g a g g a a a a	c t g g c a a g a a	600
a c t g a a a g c t	t t t a t g g c g g	t a g g g c t c t t	a a g a a a g a c a	c a a a c a t g a a	g c c t t g t t a t	660
g g c t c a t t t g	c c a g a c c t a c	c a a t g a a a a g	g g a g g t c a a g	c t a a a c t t a a	a g t t g g a g c t	720
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a a c t a t t g c t	t c c c c c t g g a	t g g g t c t g g c	a c t a a c g c c g	c t t a c c a a g g	t g t g a a a g t a	1260
a a a a a t g g t c	a a g a t g g t g a	t g t t g a g a g c	g a a t g g g a a a	a a g a t g a t a c	t g t c g c a g c t	1320
c g a a a t c a a t	t a t g c a a g g g	c a a c a t t t t t	g c c a t g g a g a	t c a a t c t c c a	g g c c a a c c t g	1380
t g g a g a a g t t	t t c t c t a c t c	g a a c g t g g c c	c t g t a c c t g c	c c g a t t c t t a	c a a g t a c a c g	1440
c c g g c c a a c a	t c a c c c t g c c	c a c c a a c a c c	a a c a c c t a c g	a t t a c a t g a a	c g g g a g a g t g	1500
g t g c c t c c c t	c g c t g g t g g a	c g c c t a c a t c	a a c a t c g g g g	c g c g c t g g t c	g c t g g a c c c c	1560
a t g g a c a a c g	t c a a t c c c t t	c a a c c a c c a t	c g c a a c g c g g	g g c t g c g c t a	c c g c t c c a t g	1620
c t c c t g g g c a	a c g g g c g c t a	c g t g c c c t t c	c a c a t c c a g g	t g c c c c a g a a	a t t t t t c g c c	1680
a t t a a g a g c c	t c c t g c t c c t	g c c c g g g t c c	t a c a c c t a c g	a g t g g a a c t t	c c g c a a g g a c	1740
g t c a a c a t g a	t c c t g c a g a g	c t c c c t c g g c	a a c g a c c t g c	g c a c g g a c g g	g g c c t c c a t c	1800
t c c t t c a c c a	g c a t c a a c c t	c t a c g c c a c c	t t c t t c c c c a	t g g c g c a c a a	c a c c g c c t c c	1860
a c g c t c a g a g	c c a t g c t g c g	c a a c g a c a c c	a a c g a c c a g t	c c t t c a a c g a	c t a c c t c t c g	1920
g c g g c c a a c a	t g c t c t a c c c	c a t c c c g g c c	a a c g c c a c c a	a c g t g c c c a t	c t c c a t c c c c	1980
t c g c g c a a c t	g g g c g c g c c t	c c g c g g c t g g	t c c t t c a c g c	g c c t c a a g a c	c a a g g a g a c g	2040

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&lt;210&gt; 24

&lt;211&gt; 2883

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 17 Hexon

&lt;400&gt; 24

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2883

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&lt;210&gt; 25

&lt;211&gt; 2877

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 19 Hexon

&lt;400&gt; 25

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<210> 30

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<212> DNA

<213> Artificial Sequence

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<223> Oligomer

<400> 30

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<210> 31

<211> 44

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligomer

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<210> 32

<211> 33

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<210> 33

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<211> 2880

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 3 Hexon

<400> 41

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&lt;210&gt; 42

&lt;211&gt; 1683

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 3 Fiber

&lt;400&gt; 42

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caa 1683

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&lt;210&gt; 43

&lt;211&gt; 2859

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 6 Hexon

&lt;400&gt; 43

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atgtatgtcc gccgaccaga aggaagagggc gcgtcgccga gttgcaagat ggccacccca 60
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&lt;210&gt; 44

&lt;211&gt; 1335

&lt;212&gt; DNA

<213> Chimpanzee Adenovirus- ChAd 6 Fiber

<400> 44

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gctgtCaccc tcaagctggg ggaggggggtg gacctcgacg actcgggaaa actcatctcc 240
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tacatTgcta aagaa                                     1335

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<210> 45

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 45

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<210> 46

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer

<400> 46

gtggaarggc acgtagcg 18

<210> 47

<211> 9

<212> PRT

<213> HIV gag CD8 Epitope

<220>

&lt;223&gt; Primer

&lt;400&gt; 47

Ala Met Gln Met Leu Lys Glu Thr Ile  
 1 5

&lt;210&gt; 48

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 20 Fiber

&lt;400&gt; 48

Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro  
 1 5 10 15  
 Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro  
 20 25 30  
 Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45  
 Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu  
 50 55 60  
 Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser  
 65 70 75 80  
 Gln Asp Ile Thr Thr Ala Ser Pro Pro Leu Lys Lys Thr Lys Thr Asn  
 85 90 95  
 Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala  
 100 105 110  
 Leu Thr Val Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu  
 115 120 125  
 Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr  
 130 135 140  
 Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu  
 145 150 155 160  
 Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val  
 165 170 175  
 Ser Ala Thr Pro Pro Leu Ser Thr Ser Asn Gly Ser Leu Gly Ile Asp  
 180 185 190  
 Met Gln Ala Pro Ile Tyr Thr Thr Asn Gly Lys Leu Gly Leu Asn Phe  
 195 200 205  
 Gly Ala Pro Leu His Val Val Asp Ser Leu Asn Ala Leu Thr Val Val  
 210 215 220  
 Thr Gly Gln Gly Leu Thr Ile Asn Gly Thr Ala Leu Gln Thr Arg Val  
 225 230 235 240  
 Ser Gly Ala Leu Asn Tyr Asp Thr Ser Gly Asn Leu Glu Leu Arg Ala  
 245 250 255  
 Ala Gly Gly Met Arg Val Asp Ala Asn Asn Gly Gln Leu Ile Leu Asp Val  
 260 265 270  
 Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln  
 275 280 285  
 Gly Pro Leu Phe Val Asn Ser Ala His Asn Leu Asp Val Asn Tyr Asn  
 290 295 300  
 Arg Gly Leu Tyr Leu Phe Thr Ser Gly Asn Thr Lys Lys Leu Glu Val  
 305 310 315 320

Asn Ile Lys Thr Ala Lys Gly Leu Ile Tyr Asp Asp Thr Ala Ile Ala  
 325 330 335  
 Ile Asn Ala Gly Asp Gly Leu Gln Phe Asp Ser Gly Ser Asp Thr Asn  
 340 345 350  
 Pro Leu Lys Thr Lys Leu Gly Leu Gly Leu Asp Tyr Asp Ser Ser Arg  
 355 360 365  
 Ala Ile Ile Ala Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly  
 370 375 380  
 Ala Ile Thr Val Gly Asn Lys Asn Asp Asp Lys Leu Thr Leu Trp Thr  
 385 390 395 400  
 Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile Tyr Ser Glu Lys Asp Ala  
 405 410 415  
 Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val Leu Ala Ser  
 420 425 430  
 Val Ser Val Leu Ser Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr  
 435 440 445  
 Val Thr Ser Ala Gln Ile Val Leu Arg Phe Asp Glu Asn Gly Val Leu  
 450 455 460  
 Leu Ser Asn Ser Ser Leu Asp Pro Gln Tyr Trp Asn Tyr Arg Lys Gly  
 465 470 475 480  
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro  
 485 490 495  
 Asn Leu Thr Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Ser Asn  
 500 505 510  
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr  
 515 520 525  
 Leu-Thr Ile Thr Leu Asn Gly Thr Asn Glu Thr Gly Asp Ala Thr Val  
 530 535 540  
 Ser Thr Tyr Ser Met Ser Phe Ser Trp Asn Trp Asn Gly Ser Asn Tyr  
 545 550 555 560  
 Ile Asn Glu Thr Phe Gln Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala  
 565 570 575  
 Gln Glu

&lt;210&gt; 49

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 4 Fiber

&lt;400&gt; 49

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60  
 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu  
 100 105 110



Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu  
 115 120 125  
 Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser  
 130 135 140  
 Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly  
 145 150 155 160  
 Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp  
 165 170 175  
 Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp  
 180 185 190  
 Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser  
 195 200 205  
 Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu  
 210 215 220  
 Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn  
 225 230 235 240  
 Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro  
 245 250 255  
 Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu  
 260 265 270  
 Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val  
 275 280 285  
 Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln  
 290 295 300  
 Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser  
 305 310 315 320  
 Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly  
 325 330 335  
 Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr  
 340 345 350  
 Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val  
 355 360 365  
 Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu  
 370 375 380  
 Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr  
 385 390 395 400  
 Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser  
 405 410 415  
 Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  
 420 425

&lt;210&gt; 50

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 5 Fiber

&lt;400&gt; 50

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60

Lys Leu Gly Asp Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu  
 100 105 110  
 Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu  
 115 120 125  
 Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn  
 130 135 140  
 Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala  
 145 150 155 160  
 Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala  
 165 170 175  
 Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr  
 180 185 190  
 Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe  
 195 200 205  
 Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln  
 210 215 220  
 Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Ser Leu  
 225 230 235 240  
 Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile  
 245 250 255  
 Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala  
 260 265 270  
 Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu  
 275 280 285  
 Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser  
 290 295 300  
 Leu Leu Ala Val Ser Gly Ser Leu Ala Pro Ile Thr Gly Ala Val Arg  
 305 310 315 320  
 Thr Ala Leu Val Ser Leu Lys Phe Asn Ala Asn Gly Ala Leu Leu Asp  
 325 330 335  
 Lys Ser Thr Leu Asn Lys Glu Tyr Trp Asn Tyr Arg Gln Gly Asp Leu  
 340 345 350  
 Ile Pro Gly Thr Pro Tyr Thr His Ala Val Gly Phe Met Pro Asn Lys  
 355 360 365  
 Lys Ala Tyr Pro Lys Asn Thr Thr Ala Ala Ser Lys Ser His Ile Val  
 370 375 380  
 Gly Asp Val Tyr Leu Asp Gly Asp Ala Asp Lys Pro Leu Ser Leu Ile  
 385 390 395 400  
 Ile Thr Phe Asn Glu Thr Asp Asp Glu Thr Cys Asp Tyr Cys Ile Asn  
 405 410 415  
 Phe Gln Trp Lys Trp Gly Ala Asp Gln Tyr Lys Asp Lys Thr Leu Ala  
 420 425 430  
 Thr Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  
 435 440

&lt;210&gt; 51

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 7 Fiber

&lt;400&gt; 51

Met	Ser	Lys	Lys	Arg	Val	Arg	Val	Asp	Asp	Asp	Phe	Asp	Pro	Val	Tyr
1				5				10						15	
Pro	Tyr	Asp	Ala	Asp	Asn	Ala	Pro	Thr	Val	Pro	Phe	Ile	Asn	Pro	Pro
			20					25					30		
Phe	Val	Ser	Ser	Asp	Gly	Phe	Gln	Glu	Lys	Pro	Leu	Gly	Val	Leu	Ser
		35				40						45			
Leu	Arg	Leu	Ala	Asp	Pro	Val	Thr	Thr	Lys	Asn	Gly	Glu	Ile	Thr	Leu
	50					55					60				
Lys	Leu	Gly	Glu	Gly	Val	Asp	Leu	Asp	Ser	Ser	Gly	Lys	Leu	Ile	Ser
65					70					75					80
Asn	Thr	Ala	Thr	Lys	Ala	Ala	Ala	Pro	Leu	Ser	Phe	Ser	Asn	Asn	Thr
				85					90					95	
Ile	Ser	Leu	Asn	Met	Asp	Thr	Pro	Phe	Tyr	Asn	Asn	Asn	Gly	Lys	Leu
			100					105					110		
Gly	Met	Lys	Val	Thr	Ala	Pro	Leu	Lys	Ile	Leu	Asp	Thr	Asp	Leu	Leu
		115					120					125			
Lys	Thr	Leu	Val	Val	Ala	Tyr	Gly	Gln	Gly	Leu	Gly	Thr	Asn	Thr	Thr
	130					135					140				
Gly	Ala	Leu	Val	Ala	Gln	Leu	Ala	Ala	Pro	Leu	Ala	Phe	Asp	Ser	Asn
145					150					155					160
Ser	Lys	Ile	Ala	Leu	Asn	Leu	Gly	Asn	Gly	Pro	Leu	Lys	Val	Asp	Ala
				165					170					175	
Asn	Arg	Leu	Asn	Ile	Asn	Cys	Asn	Arg	Gly	Leu	Tyr	Val	Thr	Thr	Thr
			180					185					190		
Lys	Asp	Ala	Leu	Glu	Thr	Asn	Ile	Ser	Trp	Ala	Asn	Ala	Met	Thr	Phe
		195					200					205			
Ile	Gly	Asn	Ala	Met	Gly	Val	Asn	Ile	Asp	Thr	Gln	Lys	Gly	Leu	Gln
	210					215					220				
Phe	Gly	Thr	Thr	Ser	Thr	Val	Ala	Asp	Val	Lys	Asn	Ala	Tyr	Pro	Ile
225					230					235					240
Gln	Val	Lys	Leu	Gly	Ala	Gly	Leu	Thr	Phe	Asp	Ser	Thr	Gly	Ala	Ile
				245					250					255	
Val	Ala	Trp	Asn	Lys	Glu	Asp	Asp	Lys	Leu	Thr	Leu	Trp	Thr	Thr	Ala
			260					265					270		
Asp	Pro	Ser	Pro	Asn	Cys	His	Ile	Tyr	Ser	Asp	Lys	Asp	Ala	Lys	Leu
		275					280					285			
Thr	Leu	Cys	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Gly	Thr	Val	Ser
	290					295					300				
Leu	Ile	Ala	Val	Asp	Thr	Gly	Ser	Leu	Asn	Pro	Ile	Thr	Gly	Gln	Val
305					310					315					320
Thr	Thr	Ala	Leu	Val	Ser	Leu	Lys	Phe	Asp	Ala	Asn	Gly	Val	Leu	Gln
				325					330					335	
Thr	Ser	Ser	Thr	Leu	Asp	Lys	Glu	Tyr	Trp	Asn	Phe	Arg	Lys	Gly	Asp
			340					345					350		
Val	Thr	Pro	Ala	Glu	Pro	Tyr	Thr	Asn	Ala	Ile	Gly	Phe	Met	Pro	Asn
		355					360					365			
Leu	Lys	Ala	Tyr	Pro	Lys	Asn	Thr	Ser	Gly	Ala	Ala	Lys	Ser	His	Ile
	370					375					380				
Val	Gly	Lys	Val	Tyr	Leu	His	Gly	Asp	Thr	Asp	Lys	Pro	Leu	Asp	Leu
385					390					395					400
Ile	Ile	Thr	Phe	Asn	Glu	Thr	Ser	Asp	Glu	Ser	Cys	Thr	Tyr	Cys	Ile
				405					410					415	
Asn	Phe	Gln	Trp	Lys	Trp	Asp	Ser	Thr	Lys	Tyr	Thr	Gly	Glu	Thr	Leu
			420					425					430		

Ala Thr Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  
 435 440 445

<210> 52

<211> 425

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 9 Fiber

<400> 52

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60  
 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu  
 100 105 110  
 Ala Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu  
 115 120 125  
 Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser  
 130 135 140  
 Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly  
 145 150 155 160  
 Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp  
 165 170 175  
 Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp  
 180 185 190  
 Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser  
 195 200 205  
 Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu  
 210 215 220  
 Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn  
 225 230 235 240  
 Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro  
 245 250 255  
 Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu  
 260 265 270  
 Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val  
 275 280 285  
 Gly Ser Gly Asp Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln  
 290 295 300  
 Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser  
 305 310 315 320  
 Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly  
 325 330 335  
 Thr Pro Tyr Ala Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr  
 340 345 350  
 Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val  
 355 360 365

Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu  
 370 375 380  
 Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr  
 385 390 395 400  
 Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser  
 405 410 415  
 Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  
 420 425

<210> 53

<211> 425

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 10 Fiber

<400> 53

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60  
 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu  
 100 105 110  
 Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu  
 115 120 125  
 Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser  
 130 135 140  
 Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly  
 145 150 155 160  
 Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp  
 165 170 175  
 Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp  
 180 185 190  
 Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser  
 195 200 205  
 Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu  
 210 215 220  
 Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn  
 225 230 235 240  
 Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro  
 245 250 255  
 Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu  
 260 265 270  
 Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val  
 275 280 285  
 Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln  
 290 295 300  
 Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Thr Glu His Ser  
 305 310 315 320

Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly  
 325 330 335  
 Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr  
 340 345 350  
 Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val  
 355 360 365  
 Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu  
 370 375 380  
 Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr  
 385 390 395 400  
 Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser  
 405 410 415  
 Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  
 420 425

&lt;210&gt; 54

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 11 Fiber

&lt;400&gt; 54

Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro  
 1 5 10 15  
 Tyr Asp Thr Glu Asn Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro  
 20 25 30  
 Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45  
 Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu  
 50 55 60  
 Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser  
 65 70 75 80  
 Gln Asp Val Thr Thr Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn  
 85 90 95  
 Leu Ser Leu Glu Thr Ser Ala Pro Leu Thr Val Ser Thr Ser Gly Ala  
 100 105 110  
 Leu Thr Leu Ala Ala Ala Val Pro Leu Ala Val Ala Gly Thr Ser Leu  
 115 120 125  
 Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr  
 130 135 140  
 Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu  
 145 150 155 160  
 Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Ile  
 165 170 175  
 Ser Ala Thr Pro Pro Leu Ser Thr Ser Asn Gly Ser Leu Gly Ile Asp  
 180 185 190  
 Met Gln Ala Pro Ile Tyr Thr Thr Asn Gly Lys Leu Gly Leu Asn Phe  
 195 200 205  
 Gly Ala Pro Leu His Val Val Asp Ser Leu Asn Ala Leu Thr Val Val  
 210 215 220  
 Thr Gly Gln Gly Leu Thr Ile Asn Gly Thr Ala Leu Gln Thr Arg Val  
 225 230 235 240  
 Ser Gly Ala Leu Asn Tyr Asp Ser Ser Gly Asn Leu Glu Leu Arg Ala  
 245 250 255  
 Ala Gly Gly Met Arg Val Asp Ala Asn Gly Lys Leu Ile Leu Asp Val  
 260 265 270

Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln  
 275 280 285  
 Gly Pro Leu Phe Val Asn Ser Ala His Asn Leu Asp Val Asn Tyr Asn  
 290 295 300  
 Arg Gly Leu Tyr Leu Phe Thr Ser Gly Asn Thr Lys Lys Leu Glu Val  
 305 310 315 320  
 Asn Ile Lys Thr Ala Lys Gly Leu Ile Tyr Asp Asp Thr Ala Ile Ala  
 325 330 335  
 Ile Asn Pro Gly Asp Gly Leu Glu Phe Gly Ser Gly Ser Asp Thr Asn  
 340 345 350  
 Pro Leu Lys Thr Lys Leu Gly Leu Gly Leu Glu Tyr Asp Ser Ser Arg  
 355 360 365  
 Ala Ile Ile Ala Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly  
 370 375 380  
 Ala Ile Thr Val Gly Asn Lys Asn Asp Asp Lys Leu Thr Leu Trp Thr  
 385 390 395 400  
 Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile Tyr Ser Glu Lys Asp Ala  
 405 410 415  
 Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val Leu Ala Ser  
 420 425 430  
 Val Ser Val Leu Ser Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr  
 435 440 445  
 Val Thr Ser Ala Gln Ile Ile Leu Arg Phe Asp Glu Asn Gly Val Leu  
 450 455 460  
 Leu Ser Asn Ser Ser Leu Asp Pro Gln Tyr Trp Asn Tyr Arg Lys Gly  
 465 470 475 480  
 Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro  
 485 490 495  
 Asn Leu Thr Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Ser Asn  
 500 505 510  
 Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Ile  
 515 520 525  
 Leu Thr Ile Thr Leu Asn Gly Thr Asn Glu Thr Gly Asp Ala Thr Val  
 530 535 540  
 Ser Thr Tyr Ser Met Ser Phe Ser Trp Asn Trp Asn Gly Ser Asn Tyr  
 545 550 555 560  
 Ile Asn Glu Thr Phe Gln Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala  
 565 570 575  
 Gln Glu

&lt;210&gt; 55

&lt;211&gt; 442

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 16 Fiber

&lt;400&gt; 55

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60



Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Thr Lys Asp Gly Lys Leu  
 100 105 110  
 Thr Met Gln Val Thr Ala Pro Leu Lys Leu Ala Asn Thr Ala Ile Leu  
 115 120 125  
 Asn Thr Leu Ala Met Ala Tyr Gly Asn Gly Leu Gly Leu Ser Asn Asn  
 130 135 140  
 Ala Leu Thr Val Gln Leu Gln Ser Pro Leu Thr Phe Asn Asn Ser Lys  
 145 150 155 160  
 Val Ala Ile Asn Leu Gly Asn Gly Pro Leu Asn Val Thr Ser Asn Arg  
 165 170 175  
 Leu Ser Ile Asn Cys Lys Arg Gly Val Tyr Val Thr Thr Thr Gly Asp  
 180 185 190  
 Ala Ile Glu Thr Asn Ile Ser Trp Ser Asn Ala Ile Lys Phe Ile Gly  
 195 200 205  
 Asn Ala Met Gly Val Asn Ile Asp Thr Asn Lys Gly Leu Gln Phe Gly  
 210 215 220  
 Thr Thr Ser Thr Val Thr Asp Val Thr Asn Ala Phe Pro Ile Gln Val  
 225 230 235 240  
 Lys Leu Gly Ala Gly Leu Ala Phe Asp Ser Thr Gly Ala Ile Val Ala  
 245 250 255  
 Trp Asn Lys Glu Asp Asp Ser Leu Thr Leu Trp Thr Thr Pro Asp Pro  
 260 265 270  
 Ser Pro Asn Cys Lys Ile Ala Ser Asp Lys Asp Ala Lys Leu Thr Leu  
 275 280 285  
 Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser Leu Leu  
 290 295 300  
 Ala Val Ser Gly Ser Leu Ala Pro Ile Thr Gly Ala Val Ser Thr Ala  
 305 310 315 320  
 Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Ala Leu Leu Glu Lys Ser  
 325 330 335  
 Thr Leu Asn Arg Glu Tyr Trp Asn Tyr Arg Gln Gly Asp Leu Ile Pro  
 340 345 350  
 Gly Thr Pro Tyr Thr His Ala Val Gly Phe Met Pro Asn Lys Lys Ala  
 355 360 365  
 Tyr Pro Lys Asn Thr Thr Ala Ala Ser Lys Ser His Ile Val Gly Glu  
 370 375 380  
 Val Tyr Leu Asp Gly Asp Ala Asp Lys Pro Leu Ser Leu Ile Ile Thr  
 385 390 395 400  
 Phe Asn Glu Thr Asp Asp Glu Ser Cys Asp Tyr Cys Met Asn Phe Gln  
 405 410 415  
 Trp Lys Trp Gly Ala Asp Gln Tyr Lys Asp Lys Thr Leu Ala Thr Ser  
 420 425 430  
 Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  
 435 440

&lt;210&gt; 56

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 17 Fiber

&lt;400&gt; 56

Met	Lys	Arg	Thr	Lys	Thr	Ser	Asp	Glu	Ser	Phe	Asn	Pro	Val	Tyr	Pro
1				5					10					15	
Tyr	Asp	Thr	Glu	Ser	Gly	Pro	Pro	Ser	Val	Pro	Phe	Leu	Thr	Pro	Pro
			20					25					30		
Phe	Val	Ser	Pro	Asp	Gly	Phe	Gln	Glu	Ser	Pro	Pro	Gly	Val	Leu	Ser
		35				40						45			
Leu	Asn	Leu	Ala	Glu	Pro	Leu	Val	Thr	Ser	His	Gly	Met	Leu	Ala	Leu
	50					55				60					
Lys	Met	Gly	Ser	Gly	Leu	Ser	Leu	Asp	Asp	Ala	Gly	Asn	Leu	Thr	Ser
65				70						75					80
Gln	Asp	Ile	Thr	Ser	Thr	Thr	Pro	Pro	Leu	Lys	Lys	Thr	Lys	Thr	Asn
				85					90						
Leu	Ser	Leu	Glu	Thr	Ser	Ser	Pro	Leu	Thr	Val	Ser	Thr	Ser	Gly	Ala
			100					105					110		
Leu	Thr	Val	Ala	Ala	Ala	Ala	Pro	Leu	Ala	Val	Ala	Gly	Thr	Ser	Leu
		115					120					125			
Thr	Met	Gln	Ser	Glu	Ala	Pro	Leu	Ala	Val	Gln	Asp	Ala	Lys	Leu	Thr
	130					135					140				
Leu	Ala	Thr	Lys	Gly	Pro	Leu	Thr	Val	Ser	Glu	Gly	Lys	Leu	Ala	Leu
145				150						155					160
Gln	Thr	Ser	Ala	Pro	Leu	Thr	Ala	Ala	Asp	Ser	Ser	Thr	Leu	Thr	Val
			165						170					175	
Ser	Ser	Thr	Pro	Pro	Ile	Ser	Val	Ser	Ser	Gly	Ser	Leu	Gly	Leu	Asp
			180					185					190		
Met	Glu	Asp	Pro	Met	Tyr	Thr	His	Asp	Gly	Lys	Leu	Gly	Ile	Arg	Ile
	195						200					205			
Gly	Gly	Pro	Leu	Arg	Val	Val	Asp	Ser	Leu	His	Thr	Leu	Thr	Val	Val
	210					215					220				
Thr	Gly	Asn	Gly	Leu	Thr	Val	Asp	Asn	Asn	Ala	Leu	Gln	Thr	Arg	Val
225				230						235					240
Thr	Gly	Ala	Leu	Gly	Tyr	Asp	Thr	Ser	Gly	Asn	Leu	Gln	Leu	Arg	Ala
			245						250					255	
Ala	Gly	Gly	Met	Arg	Ile	Asp	Ala	Asn	Gly	Gln	Leu	Ile	Leu	Asp	Val
		260					265						270		
Ala	Tyr	Pro	Phe	Asp	Ala	Gln	Asn	Asn	Leu	Ser	Leu	Arg	Leu	Gly	Gln
	275						280					285			
Gly	Pro	Leu	Tyr	Val	Asn	Thr	Asp	His	Asn	Leu	Asp	Leu	Asn	Cys	Asn
	290					295					300				
Arg	Gly	Leu	Thr	Thr	Thr	Thr	Thr	Asn	Asn	Thr	Lys	Lys	Leu	Glu	Thr
305				310						315					320
Lys	Ile	Ser	Ser	Gly	Leu	Asp	Tyr	Asp	Thr	Asn	Gly	Ala	Val	Ile	Ile
			325						330					335	
Lys	Leu	Gly	Thr	Gly	Leu	Ser	Phe	Asp	Asn	Thr	Gly	Ala	Leu	Thr	Val
		340					345						350		
Gly	Asn	Thr	Gly	Asp	Asp	Lys	Leu	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Pro
	355					360						365			
Ser	Pro	Asn	Cys	Arg	Ile	His	Ser	Asp	Lys	Asp	Cys	Lys	Phe	Thr	Leu
	370					375					380				
Val	Leu	Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Ser	Val	Ala	Ala	Leu
385				390						395					400
Ala	Val	Ser	Gly	Asn	Leu	Ala	Ser	Ile	Thr	Gly	Thr	Val	Ala	Ser	Val
			405						410					415	
Thr	Ile	Phe	Leu	Arg	Phe	Asp	Gln	Asn	Gly	Val	Leu	Met	Glu	Asn	Ser
			420					425					430		

Ser Leu Asp Lys Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn  
 435 440 445  
 Ala Ala Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala  
 450 455 460  
 Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln  
 465 470 475 480  
 Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr Leu Thr Ile Thr  
 485 490 495  
 Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr  
 500 505 510  
 Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu  
 515 520 525  
 Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln  
 530 535 540

&lt;210&gt; 57

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 19 Fiber

&lt;400&gt; 57

Met Lys Arg Thr Lys Thr Ser Asp Lys Ser Phe Asn Pro Val Tyr Pro  
 1 5 10 15  
 Tyr Asp Thr Glu Asn Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro  
 20 25 30  
 Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45  
 Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu  
 50 55 60  
 Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser  
 65 70 75 80  
 Gln Asp Val Thr Thr Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn  
 85 90 95  
 Leu Ser Leu Glu Thr Ser Ala Pro Leu Thr Val Ser Thr Ser Gly Ala  
 100 105 110  
 Leu Thr Leu Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu  
 115 120 125  
 Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr  
 130 135 140  
 Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu  
 145 150 155 160  
 Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val  
 165 170 175  
 Ser Ala Thr Pro Pro Ile Ser Val Ser Ser Gly Ser Leu Gly Leu Asp  
 180 185 190  
 Met Glu Asp Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile  
 195 200 205  
 Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val  
 210 215 220  
 Thr Gly Asn Gly Ile Ala Val Asp Asn Asn Ala Leu Gln Thr Arg Val  
 225 230 235 240  
 Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala  
 245 250 255  
 Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asp Val  
 260 265 270

Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln  
 275 280 285  
 Gly Pro Leu Tyr Val Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn  
 290 295 300  
 Arg Gly Leu Thr Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr  
 305 310 315  
 Lys Ile Gly Ser Gly Leu Asp Tyr Asp Thr Asn Gly Ala Val Ile Ile  
 325 330 335  
 Lys Leu Gly Thr Gly Val Ser Phe Asp Ser Thr Gly Ala Leu Ser Val  
 340 345 350  
 Gly Asn Thr Gly Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro  
 355 360 365  
 Ser Pro Asn Cys Arg Ile His Ser Asp Lys Asp Cys Lys Phe Thr Leu  
 370 375 380  
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Ala Leu  
 385 390 395 400  
 Ala Val Ser Gly Asn Leu Ala Ser Ile Thr Gly Thr Val Ser Ser Val  
 405 410 415  
 Thr Ile Phe Leu Arg Phe Asp Gln Asn Gly Val Leu Met Glu Asn Ser  
 420 425 430  
 Ser Leu Asp Lys Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn  
 435 440 445  
 Ala Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala  
 450 455 460  
 Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln  
 465 470 475 480  
 Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr Leu Thr Ile Thr  
 485 490 495  
 Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr  
 500 505 510  
 Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu  
 515 520 525  
 Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln  
 530 535 540

&lt;210&gt; 58

&lt;211&gt; 963

&lt;212&gt; DNA

&lt;213&gt; Chimapnzee Adenovirus- ChAd 8 Fiber

&lt;400&gt; 58

atgaccaaac gagttcgact aagcagctcc ttcaatccgg tctaccoccta tgaagatgaa 60  
 agcagctccc aacaccctt tataaacctt ggtttcattt cctcaaattg atttacacaa 120  
 agcccagatg gggttcttac acttaaattg ttatcgccgc tcaccaccac aggcggctcc 180  
 cttcaactta aagttggagg aggattatca gtggatgaca ctgacggttc attagaagaa 240  
 aacataagca ttacagcacc acttaataaaa acaagtcact caatagggtt atccatagga 300  
 gatgggttgg aaacaaaaaa caaccaacta tgtgctaagc tgggagacgg tcttacattt 360  
 aatacaggca gcatatgcat agatactgac attaatacat tatggacagg agcaacacca 420  
 gacgctaatt gcttagtcct tggaactgaa tctaattgatt gttaaacttac actggcactt 480  
 gtaaagtcag gagccttagt aaatgcttac gtagcacttg ttggagcctc agacgccgtt 540  
 aatgatttaa ccacagaaac aagtgtctcaa ataattgcag acatatattt tgatgcgcaa 600  
 ggaaaacttc ttcctgattt atcagcactc aaaacagagc taaaacacaa atctggacaa 660  
 ggcacttcga cagcagatcc caataactgt aaaagcttta tgccaagtct aaatgcatat 720  
 ccactgcgcc ccaatggagg caacggaaac tatatttatg gaaccaccta ctacagggcc 780  
 agagatgaaa ccctttatga acttaaaaacc tctgtaattg ttaactacaa aattaccagt 840

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ggactatgtg catatgccat gcatttttcag tgggtcttggga atagtggggac taaaccagaa 900
gacactcccg ccacttttcat tgcctccccc tttgtctttt cctacattag agaagatgac 960
tga 963

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&lt;210&gt; 59

&lt;211&gt; 320

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 8 Fiber

&lt;400&gt; 59

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Met Thr Lys Arg Val Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1      5      10      15
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
      20      25      30
Ile Ser Ser Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu
      35      40      45
Lys Cys Leu Ser Pro Leu Thr Thr Thr Gly Gly Ser Leu Gln Leu Lys
      50      55      60
Val Gly Gly Gly Leu Ser Val Asp Asp Thr Asp Gly Ser Leu Glu Glu
65      70      75      80
Asn Ile Ser Ile Thr Ala Pro Leu Asn Lys Thr Ser His Ser Ile Gly
      85      90      95
Leu Ser Ile Gly Asp Gly Leu Glu Thr Lys Asn Asn Gln Leu Cys Ala
      100      105      110
Lys Leu Gly Asp Gly Leu Thr Phe Asn Thr Gly Ser Ile Cys Ile Asp
      115      120      125
Thr Asp Ile Asn Thr Leu Trp Thr Gly Ala Thr Pro Asp Ala Asn Cys
130      135      140
Leu Val Leu Gly Thr Glu Ser Asn Asp Cys Lys Leu Thr Leu Ala Leu
145      150      155      160
Val Lys Ser Gly Ala Leu Val Asn Ala Tyr Val Ala Leu Val Gly Ala
      165      170      175
Ser Asp Ala Val Asn Asp Leu Thr Thr Glu Thr Ser Ala Gln Ile Ile
      180      185      190
Ala Asp Ile Tyr Phe Asp Ala Gln Gly Lys Leu Leu Pro Asp Leu Ser
      195      200      205
Ala Leu Lys Thr Glu Leu Lys His Lys Ser Gly Gln Gly Thr Ser Thr
      210      215      220
Ala Asp Pro Asn Asn Cys Lys Ser Phe Met Pro Ser Leu Asn Ala Tyr
225      230      235      240
Pro Leu Arg Pro Asn Gly Gly Asn Gly Asn Tyr Ile Tyr Gly Thr Thr
      245      250      255
Tyr Tyr Arg Ala Arg Asp Glu Thr Leu Tyr Glu Leu Lys Thr Ser Val
      260      265      270
Met Leu Asn Tyr Lys Ile Thr Ser Gly Leu Cys Ala Tyr Ala Met His
      275      280      285
Phe Gln Trp Ser Trp Asn Ser Gly Thr Lys Pro Glu Asp Thr Pro Ala
      290      295      300
Thr Phe Ile Ala Ser Pro Phe Val Phe Ser Tyr Ile Arg Glu Asp Asp
305      310      315      320

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&lt;210&gt; 60

&lt;211&gt; 1062

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 22 Fiber

&lt;400&gt; 60

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atggccaaac gagctcgggt aagcagctcc ttcaatccgg tctacccta tgaagatgaa 60
agcagctcac aacacccctt tataaaccct ggtttcattt cctcaaattg ttttgcacaa 120
agccagatg gagttctaac tcttaaattg gttaatccgc tctactaccgc cagcggaccc 180
ctccaactta aagttggaag cagtcttaca gtagataata tcgatgggtc tttggaggaa 240
aatataactg ccgcagcgcc actcactaaa actaaccact ccatagggtt atcaatagga 300
tctggccttg aaacaaagga tgataaactt tgtttatcgc tgggagatgg gttggtaaca 360
aaggatgata aactatgttt atcgctggga gatgggttaa taacaaaaga tgatacacta 420
tgtgccaaac taggacatgg ccttggtgtt gactcttcca atgctatcac catagaaaac 480
aacaccttgt ggacaggtgc aaaaccaagc gccaaactgt taattaaaga gggagaagat 540
tccccagact gtaagctcac tttagttcta gtgaagaatg gaggactgat aaatggatac 600
ataacattaa tgggagcctc agaataact aacaccttgt ttaaaaacaa acaagttaca 660
atcgatgtaa acctcgcat tgataatact ggccaaatta tcaattacct atcatccctt 720
aaaagtaacc tgaactttta agacaaccaa aacatgggta ctggaaccat aaccagtgcc 780
aaaggcttca tgcccagcac caccgcctat ccatttataa catacgccac tcagtcctta 840
aatgaagatt acatttatgg agagtgttac tacaaatcta ccaatggaac tctctttcca 900
ctaaaagtta ctgtcacact aaacagacgt atgtcagctt ctggaatggc ctatgctatg 960
aatttttcat ggtctctaaa tgcagaggaa gccccggaaa ctaccgaagt cactctcatt 1020
acctccccct tctttttttc ttatatcaga gaagatgact ga 1062

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&lt;210&gt; 61

&lt;211&gt; 353

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 22 Fiber

---&lt;400&gt; 61

```

Met Ala Lys Arg Ala Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
1      5      10      15
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
20     25     30
Ile Ser Ser Asn Gly Phe Ala Gln Ser Pro Asp Gly Val Leu Thr Leu
35     40     45
Lys Cys Val Asn Pro Leu Thr Thr Ala Ser Gly Pro Leu Gln Leu Lys
50     55     60
Val Gly Ser Ser Leu Thr Val Asp Asn Ile Asp Gly Ser Leu Glu Glu
65     70     75     80
Asn Ile Thr Ala Ala Ala Pro Leu Thr Lys Thr Asn His Ser Ile Gly
85     90     95
Leu Ser Ile Gly Ser Gly Leu Gln Thr Lys Asp Asp Lys Leu Cys Leu
100    105    110
Ser Leu Gly Asp Gly Leu Val Thr Lys Asp Asp Lys Leu Cys Leu Ser
115    120    125
Leu Gly Asp Gly Leu Ile Thr Lys Asp Asp Thr Leu Cys Ala Lys Leu
130    135    140
Gly His Gly Leu Val Phe Asp Ser Ser Asn Ala Ile Thr Ile Glu Asn
145    150    155    160
Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile Lys
165    170    175
Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val Lys
180    185    190
Asn Gly Gly Leu Ile Asn Gly Tyr Ile Thr Leu Met Gly Ala Ser Glu
195    200    205
Tyr Thr Asn Thr Leu Phe Lys Asn Lys Gln Val Thr Ile Asp Val Asn
210    215    220

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Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser Leu  
 225 230 235 240  
 Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly Thr  
 245 250 255  
 Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Phe  
 260 265 270  
 Ile Thr Tyr Ala Thr Gln Ser Leu Asn Glu Asp Tyr Ile Tyr Gly Glu  
 275 280 285  
 Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val Thr  
 290 295 300  
 Val Thr Leu Asn Arg Arg Met Ser Ala Ser Gly Met Ala Tyr Ala Met  
 305 310 315 320  
 Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr Glu  
 325 330 335  
 Val Thr Leu Ile Thr Ser Pro Phe Phe Phe Ser Tyr Ile Arg Glu Asp  
 340 345 350  
 Asp

&lt;210&gt; 62

&lt;211&gt; 1686

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 24 Fiber

&lt;400&gt; 62

atgtcagatt cttgctcctg tccttccgca cccactatct tcatgttggt gcagatgaag 60  
 cgcaccaaaaa cgtctgacga gagcttcaac cccgtgtacc cctatgacac ggaaaacggt 120  
 cctccctccg tccctttcct caccctccc ttcgtgtctc ccgatggatt ccaagagagc 180  
 cccccggggg tcctgtctct gaacctggcc gagccctgg tcaacttccca cggcatgctc 240  
 gccctgaaaa tgggaagtgg cctctccctg gacgacgccg gcaacctcac ctctcaagat 300  
 gtccaccacca ctaccctccc cctgaaaaaa accaagacca acctcagcct agaaacctca 360  
 gccccctga ctgtgagcac ctcaggcgcc ctcaccctag cggcgcgcgc tcccctggcg 420  
 gtggccggca cctccctcac catgcaatca gagggccccc tgacagtaca ggatgcaaaa 480  
 ctcaccctgg ccaccaaggg cccctgacc gtgtctgaag gcaaactggc cttgcagacc 540  
 tcggccccc tgacggccgc tgacagcagc accctcaccg ttagcgccac accacccatc 600  
 aatgtaagca gtggaagttt gggcttagac atggaaaatc ccatgtatac tcatgacgga 660  
 aaactgggaa taagaattgg gggccactg agagtagtag acagcctgca cacactgact 720  
 gtagttaccg gaaatggaat agctgtagat aacaatgccc tccaaactag agttacgggc 780  
 gccctggggt atgacacatc aggaaacct caactgagag ccgcgggggg tatgcgaatt 840  
 gatgcaaatg gccaacttat ccttgatgtg gcatacccat ttgatgtctc aaacaatctc 900  
 agccttagac ttggtcaggg acccctgtat gtaaacacag accacaacct agatttgaat 960  
 tgcaacagag gtctgaccac aactaccacc aacaacacaa aaaaacttga aactaaaatt 1020  
 ggctcagggt tagactatga taccaatggt gctgtcatta ttaaacttgg cactggtgtc 1080  
 agctttgaca gcacaggcgc cctaagtgtg ggaaacactg gcgatgataa actgactctg 1140  
 tggacaaccc cagacccatc tccaaattgc agaattcact cagacaaaga ctgcaagttt 1200  
 actctagtcc taactaagtg tggaagtcaa atcctggcct ctgtcgccgc cctagcgggtg 1260  
 tcaggaaatc tggcttcaat aacaggcacc gtttccagcg ttaccatctt tctcagattt 1320  
 gatcagaatg gagggttat ggaaaactcc tcgctagaca agcagtactg gaactttaga 1380  
 aatggtaatt caaccaatgc caccctctac accaatgcag ttgggtttcat gccaaacctc 1440  
 gcagcatacc ccaagacaca gagtccagact gctaaaaaca acattgtaag tcagggtttac 1500  
 ttgaatgggg acaaatccaa acccatgatc cttaccatta ccctcaatgg aactaatgaa 1560  
 tccagtgaat ctagccagggt gagtccactac tccatgtcat ttacgtgggc ttgggagagt 1620  
 gggcaatatg ccaccgaaac ctttgccacc aattccttta ctttctctta cattgctgaa 1680  
 caataa 1686

&lt;210&gt; 63



<211> 543  
 <212> PRT  
 <213> Chimpanzee Adenovirus- ChAd 24 Fiber

<400> 63  
 Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro  
 1 5 10 15  
 Tyr Asp Thr Glu Asn Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro  
 20 25 30  
 Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45  
 Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu  
 50 55 60  
 Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser  
 65 70 75 80  
 Gln Asp Val Thr Thr Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn  
 85 90 95  
 Leu Ser Leu Glu Thr Ser Ala Pro Leu Thr Val Ser Thr Ser Gly Ala  
 100 105 110  
 Leu Thr Leu Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu  
 115 120 125  
 Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr  
 130 135 140  
 Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu  
 145 150 155 160  
 Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val  
 165 170 175  
 Ser Ala Thr Pro Pro Ile Asn Val Ser Ser Gly Ser Leu Gly Leu Asp  
 180 185 190  
 Met Glu Asn Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile  
 195 200 205  
 Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val  
 210 215 220  
 Thr Gly Asn Gly Ile Ala Val Asp Asn Asn Ala Leu Gln Thr Arg Val  
 225 230 235 240  
 Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala  
 245 250 255  
 Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asp Val  
 260 265 270  
 Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln  
 275 280 285  
 Gly Pro Leu Tyr Val Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn  
 290 295 300  
 Arg Gly Leu Thr Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr  
 305 310 315 320  
 Lys Ile Gly Ser Gly Leu Asp Tyr Asp Thr Asn Gly Ala Val Ile Ile  
 325 330 335  
 Lys Leu Gly Thr Gly Val Ser Phe Asp Ser Thr Gly Ala Leu Ser Val  
 340 345 350  
 Gly Asn Thr Gly Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro  
 355 360 365  
 Ser Pro Asn Cys Arg Ile His Ser Asp Lys Asp Cys Lys Phe Thr Leu  
 370 375 380  
 Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Ala Leu  
 385 390 395 400

Ala Val Ser Gly Asn Leu Ala Ser Ile Thr Gly Thr Val Ser Ser Val  
 405 410 415  
 Thr Ile Phe Leu Arg Phe Asp Gln Asn Gly Val Leu Met Glu Asn Ser  
 420 425 430  
 Ser Leu Asp Lys Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn  
 435 440 445  
 Ala Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala  
 450 455 460  
 Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln  
 465 470 475 480  
 Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Ile Leu Thr Ile Thr  
 485 490 495  
 Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr  
 500 505 510  
 Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu  
 515 520 525  
 Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln  
 530 535 540

&lt;210&gt; 64

&lt;211&gt; 1335

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 26 Fiber

&lt;400&gt; 64

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atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtgct gtccctgcgt ctggccgatc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agatgggggtg gacctcgacg actcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgcccctctc agtttttcca acaacaccat ttcccttaac 300
atggataccc ctctttacaa caacaatgga aagctaggta tgaaggtaac cgcaccatta 360
aagatattag acacagatct actaaaaaca cttgttggtg cttatgggca gggattagga 420
acaaacacca atgggtgctct tgttgcccaa ctagcatacc cacttgtttt taataccgct 480
agcaaaattg cccttaattt aggcaatgga ccattaaaag tggatgcaaa tagactgaac 540
attaattgca aaagagggtat ctatgtcact accacaaaag atgcactgga gattaatatc 600
agttggggcaa atgctatgac atttatagga aatgccattg gtgtcaatat tgacacaaaa 660
aaaggcctac agttcggcac ttcaagcact gaaacagatg ttaaaaatgc ttttccactc 720
caagtaaaac ttggagctgg tcttacattt gacagcacag gtgccattgt tgcttggaac 780
aaagaagatg acaaacttac actgtggacc acagccgatc catctccaaa ctgtcacata 840
tattctgcaa aggatgctaa gcttacactc tgcttgacaa agtgtggtag tcaaatccta 900
ggcactgtct ccctattagc agtcagtggc agcttggctc ctatcacagg ggctgttaga 960
actgcacttg tatcactcaa attcaatgct aatggagccc ttttggacaa atcaactctg 1020
aacaagaat actggaacta cagacaagga gatctaattc caggtacacc atatacacat 1080
gctgtggggtt tcatgcctaa caaaaaagcc taccctaaaa acacaactgc agcttccaag 1140
agccacattg tgggtgatgt gtatttagat ggagatgcag ataaaccttt atctcttatc 1200
atcactttca atgaaactga tgatgaaacc tgtgattact gcatcaactt tcaatggaaa 1260
tggggagctg atcaatataa ggataagaca ctgcgaacca gttcattcac cttctcatac 1320
atgcaccaag aataa                                     1335

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&lt;210&gt; 65

&lt;211&gt; 444

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 26 Fiber

&lt;400&gt; 65

```

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1      5      10      15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
      20      25      30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
      35      40      45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
      50      55      60
Lys Leu Gly Asp Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser
65      70      75      80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
      85      90      95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu
      100      105      110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
      115      120      125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn
130      135      140
Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala
145      150      155      160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
      165      170      175
Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr
      180      185      190
Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
      195      200      205
Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln
210      215      220
Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Pro Leu
225      230      235      240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
      245      250      255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
      260      265      270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu
      275      280      285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
290      295      300
Leu Leu Ala Val Ser Gly Ser Leu Ala Pro Ile Thr Gly Ala Val Arg
305      310      315      320
Thr Ala Leu Val Ser Leu Lys Phe Asn Ala Asn Gly Ala Leu Leu Asp
      325      330      335
Lys Ser Thr Leu Asn Lys Glu Tyr Trp Asn Tyr Arg Gln Gly Asp Leu
      340      345      350
Ile Pro Gly Thr Pro Tyr Thr His Ala Val Gly Phe Met Pro Asn Lys
      355      360      365
Lys Ala Tyr Pro Lys Asn Thr Thr Ala Ala Ser Lys Ser His Ile Val
      370      375      380
Gly Asp Val Tyr Leu Asp Gly Asp Ala Asp Lys Pro Leu Ser Leu Ile
385      390      395      400
Ile Thr Phe Asn Glu Thr Asp Asp Glu Thr Cys Asp Tyr Cys Ile Asn
      405      410      415
Phe Gln Trp Lys Trp Gly Ala Asp Gln Tyr Lys Asp Lys Thr Leu Ala
      420      425      430

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Thr Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  
 435 440

<210> 66

<211> 1062

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 30 Fiber

<400> 66

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atggccaaac gagctcgggt aagcagctcc ttcaatccgg tctacccta tgaagatgaa 60
agcagctcac aacaccctt tataaacctt ggtttcattt cctcaaattg ttttgcacaa 120
agcccagatg gagttctaac tcttaaattg gttaatccgc tctactaccgc cagcggaccc 180
ctccaactta aagttggaag cagtcttaca gtagatacta tcgatgggtc tttggaggaa 240
aatataactg ccgcagcgcc actcactaaa actaaccact ccataggttt atcaatagga 300
tctggccttg aaacaaagga tgataaacctt tgtttatcgc tgggagatgg gttggttaaca 360
aaggatgata aactatgttt atcgctggga gatgggttaa taacaaaaga tgatacacta 420
tgtgccaaac taggacatgg ccttgtgttt gactcttcca atgctatcac catagaaaac 480
aacaccttgt ggacaggtgc aaaaccaagc gccaaactgtg taattaaaga gggagaagat 540
tccccagact gtaagctcac tttagtctta gtgaagaatg gaggactgat aaatggatac 600
ataacattaa tgggagcctc agaataact aacaccttgt ttaaaaacaa acaagttaca 660
atcgatgtaa acctcgcat tggataaact ggccaaatta tcaattacct atcatccctt 720
aaaagtaacc tgaactttta agacaaccaa aacatggcta ctggaacct aaccagtgcc 780
aaaggcttca tgcccagcac caccgctat ccatttataa catacgccac tcagtcccta 840
aatgaagatt acatttatgg agagtgttac tacaaatcta ccaatggaac tctctttcca 900
ctaaaagtta ctgtcacact aaacagacgt atgtcagctt ctggaatggc ctatgctatg 960
aatttttcat ggtctctaaa tgcagaggaa gccccgaaa ctaccgaagt cactctcatt 1020
acctccccct tctttttttc ttatatcaga gaagatgact ga 1062

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<210> 67

<211> 353

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 30 Fiber

<400> 67

```

Met Ala Lys Arg Ala Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1          5          10          15
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
 20          25          30
Ile Ser Ser Asn Gly Phe Ala Gln Ser Pro Asp Gly Val Leu Thr Leu
 35          40          45
Lys Cys Val Asn Pro Leu Thr Thr Ala Ser Gly Pro Leu Gln Leu Lys
 50          55          60
Val Gly Ser Ser Leu Thr Val Asp Thr Ile Asp Gly Ser Leu Glu Glu
 65          70          75          80
Asn Ile Thr Ala Ala Ala Pro Leu Thr Lys Thr Asn His Ser Ile Gly
 85          90          95
Leu Ser Ile Gly Ser Gly Leu Gln Thr Lys Asp Asp Lys Leu Cys Leu
100          105          110
Ser Leu Gly Asp Gly Leu Val Thr Lys Asp Asp Lys Leu Cys Leu Ser
115          120          125
Leu Gly Asp Gly Leu Ile Thr Lys Asp Asp Thr Leu Cys Ala Lys Leu
130          135          140
Gly His Gly Leu Val Phe Asp Ser Ser Asn Ala Ile Thr Ile Glu Asn
145          150          155          160

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Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile Lys  
 165 170 175  
 Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val Lys  
 180 185 190  
 Asn Gly Gly Leu Ile Asn Gly Tyr Ile Thr Leu Met Gly Ala Ser Glu  
 195 200 205  
 Tyr Thr Asn Thr Leu Phe Lys Asn Lys Gln Val Thr Ile Asp Val Asn  
 210 215 220  
 Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser Leu  
 225 230 235 240  
 Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly Thr  
 245 250 255  
 Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Phe  
 260 265 270  
 Ile Thr Tyr Ala Thr Gln Ser Leu Asn Glu Asp Tyr Ile Tyr Gly Glu  
 275 280 285  
 Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val Thr  
 290 295 300  
 Val Thr Leu Asn Arg Arg Met Ser Ala Ser Gly Met Ala Tyr Ala Met  
 305 310 315 320  
 Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr Glu  
 325 330 335  
 Val Thr Leu Ile Thr Ser Pro Phe Phe Phe Ser Tyr Ile Arg Glu Asp  
 340 345 350  
 Asp

&lt;210&gt; 68

&lt;211&gt; 1791

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 31 Fiber

&lt;400&gt; 68

atgtcagatt cttgctcctg tccctccgca cccactatct tcatgttggt gcagatgaag 60  
 cgcacaaaaa cgtctgacga gagcttcaac cccgtgtacc cctatgacac ggaaagcggc 120  
 cctccctccg tccctttcct caccctccc ttcgtgtctc ccgatggatt ccaagaaagt 180  
 cccccgggg tctgtctct gaacctggcc gagcccctgg tcaattccca cggcatgctc 240  
 gccctgaaaa tgggaagtgg cctctccctg gacgacgctg gcaacctcac ctctcaagat 300  
 atcaccaccg ctagccctcc cctcaaaaaa accaagacca acctcagcct agaaacctca 360  
 tccccctaa ctgtgagcac ctccaggcgc ctcaccgtag cagccgcgcg tcccctggcg 420  
 gtggccggca cctccctcac catgcaatca gagggccccc tgacagtaca ggatgcaaaa 480  
 ctccacctgg ccaccaaagg cccctgacc gtgtctgaag gcaaactggc cttgcaaaaca 540  
 tcggccccgc tgacggccgc tgacagcagc accctcacag tcagtgccac accacctt 600  
 agcacaagca atggcagctt gggtattgac atgcaagccc ccatttacac caccaatgga 660  
 aaactaggac ttaactttgg cgctcccctg catgtggtag acagcctaaa tgcactgact 720  
 gtagttactg gccaaagtct tacgataaac ggaacagccc tacaaactag agtctcaggt 780  
 gccctcaact atgacacatc aggaaccta gaattgagag ctgcaggggg tatgcgagtt 840  
 gatgcaaatg gtcaacttat cttgatgta gcttaccat ttgatgcaca aaacaatctc 900  
 agccttaggc ttggacaggg acccctgttt gttaactctg cccacaactt ggatgttaac 960  
 tacaacagag gcctctacct gttcacatct ggaaatacca aaaagctaga agttaatatc 1020  
 aaaacagcca agggctctcat ttatgatgac actgctatag caatcaatgc ggggtgatggg 1080  
 ctacagtttg acctaggctc agatacaaat ccattaaaaa ctaaacttgg attaggactg 1140  
 gattatgact ccagcagagc cataattgct aaactgggaa ctggcctaag ctttgacaac 1200  
 acaggtgcca tcacagtagg caacaaaaat gatgacaagc ttaccttgtg gaccacacca 1260  
 gacccatccc ctaactgtag aatctattca gagaaagatg ctaaattcac acttggtttt 1320  
 actaaatgcg gcagtcaggt gttggccagc gtttctgttt tatctgtaaa aggtagcctt 1380

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gcgcccatca gtggcacagt aactagtgtc cagattgtcc tcagatttga tgaaaatgga 1440
gtttactactaa gcaattcttc ccttgaccct caatactgga actacagaaa aggtgacctt 1500
acagaggggca ctgcatatac caacgcagtg ggatttatgc ccaacctcac agcataccca 1560
aaaacacaga gccaaactgc taaaagcaac attgtaagtc aggtttactt gaatggggac 1620
aaatccaaac ccatgaccct caccattacc ctcaatggaa ctaatgaaac aggagatgcc 1680
acagtaagca cttactccat gtcattctca tggaactgga atggaagtaa ttacattaat 1740
gaaacgttcc aaaccaactc cttcaccttc tcctacatcg cccaagaata a 1791

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&lt;210&gt; 69

&lt;211&gt; 578

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 31 Fiber

&lt;400&gt; 69

```

Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
1      5      10      15
Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
20      25      30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35      40      45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
50      55      60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65      70      75      80
Gln Asp Ile Thr Thr Ala Ser Pro Pro Leu Lys Lys Thr Lys Thr Asn
85      90      95
Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala
100      105      110
Leu Thr Val Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
115      120      125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
130      135      140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145      150      155      160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
165      170      175
Ser Ala Thr Pro Pro Leu Ser Thr Ser Asn Gly Ser Leu Gly Ile Asp
180      185      190
Met Gln Ala Pro Ile Tyr Thr Thr Asn Gly Lys Leu Gly Leu Asn Phe
195      200      205
Gly Ala Pro Leu His Val Val Asp Ser Leu Asn Ala Leu Thr Val Val
210      215      220
Thr Gly Gln Gly Leu Thr Ile Asn Gly Thr Ala Leu Gln Thr Arg Val
225      230      235      240
Ser Gly Ala Leu Asn Tyr Asp Thr Ser Gly Asn Leu Glu Leu Arg Ala
245      250      255
Ala Gly Gly Met Arg Val Asp Ala Asn Gly Gln Leu Ile Leu Asp Val
260      265      270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
275      280      285
Gly Pro Leu Phe Val Asn Ser Ala His Asn Leu Asp Val Asn Tyr Asn
290      295      300
Arg Gly Leu Tyr Leu Phe Thr Ser Gly Asn Thr Lys Lys Leu Glu Val
305      310      315      320

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<210> 70
<211> 978
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 37 Fiber
```

- 101 -



cacagtggtca ttagttctct atgtgcatat gcaatgcaca tttcatgggtc atgggacacc 900  
 gtaacagagc cagagacaac acccactact cttattacct ccccttctc cttttcctat 960  
 atcagagaag atgactga 978

<210> 71

<211> 325

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 37 Fiber

<400> 71

Met	Ala	Lys	Arg	Ala	Arg	Leu	Ser	Ser	Ser	Phe	Asn	Pro	Val	Tyr	Pro	1	5	10	15
Tyr	Glu	Asp	Glu	Ser	Ser	Ser	Gln	His	Pro	Phe	Ile	Asn	Pro	Gly	Phe	20	25	30	
Ile	Ser	Pro	Asp	Gly	Phe	Thr	Gln	Ser	Pro	Asp	Gly	Val	Leu	Thr	Leu	35	40	45	
Lys	Cys	Val	Ser	Pro	Leu	Thr	Thr	Thr	Ser	Gly	Ala	Leu	Asp	Ile	Lys	50	55	60	
Val	Gly	Arg	Gly	Leu	Lys	Val	Asp	Ser	Thr	Asp	Gly	Ser	Leu	Glu	Glu	65	70	75	80
Asn	Ile	Asp	Ile	Thr	Ala	Pro	Leu	Thr	Lys	Phe	Asn	His	Ser	Val	Gly	85	90	95	
Leu	Ala	Phe	Gly	Asp	Gly	Leu	Glu	Thr	Lys	Glu	Asn	Lys	Leu	Tyr	Val	100	105	110	
Lys	Leu	Gly	Asp	Gly	Leu	Lys	Phe	Ser	Ser	Gly	Ser	Ile	Tyr	Ile	Asp	115	120	125	
His	Asp	Val	Asn	Thr	Leu	Trp	Thr	Gly	Val	Asn	Pro	Ser	Ala	Asn	Cys	130	135	140	
Ile	Ile	Thr	Asp	Asn	Gly	Glu	Thr	Asn	Asp	Ser	Lys	Leu	Thr	Leu	Ile	145	150	155	160
Leu	Val	Lys	Ser	Gly	Gly	Leu	Ile	Asn	Ala	Tyr	Val	Ser	Leu	Met	Gly	165	170	175	
Asp	Ser	Asp	Thr	Val	Asn	Lys	Leu	Thr	Glu	Lys	Ser	Ala	Gln	Ile		180	185	190	
Thr	Val	Asp	Ile	Tyr	Phe	Asp	Asn	Gln	Gly	Lys	Val	Leu	Thr	Glu	Leu	195	200	205	
Ser	Ala	Leu	Lys	Thr	Asp	Leu	Lys	His	Lys	Phe	Gly	Gln	Asn	Met	Ala	210	215	220	
Ser	Ser	Glu	Val	Ser	Asn	Cys	Lys	Gly	Phe	Met	Pro	Ser	Leu	Asn	Ala	225	230	235	240
Tyr	Pro	Phe	Arg	Asn	Pro	Thr	Lys	Pro	Thr	Lys	Gly	Arg	Glu	Asp	Tyr	245	250	255	
Ile	Tyr	Gly	Ile	Thr	Tyr	Tyr	Gln	Ala	Thr	Asp	Gly	Asn	Leu	Tyr	Glu	260	265	270	
Leu	Lys	Thr	Thr	Ile	Thr	Leu	Asn	His	Ser	Val	Ile	Ser	Ser	Leu	Cys	275	280	285	
Ala	Tyr	Ala	Met	His	Ile	Ser	Trp	Ser	Trp	Asp	Thr	Val	Thr	Glu	Pro	290	295	300	
Glu	Thr	Thr	Pro	Thr	Thr	Leu	Ile	Thr	Ser	Pro	Phe	Ser	Phe	Ser	Tyr	305	310	315	320
Ile	Arg	Glu	Asp	Asp												315	320	325	

<210> 72

<211> 1332

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 38 Fiber

&lt;400&gt; 72

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atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtggt gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agaggggggtg gacctcgact cctcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgccccctctc agtttttcca acaacacccat ttcccttaac 300
atggataccc ctttttatac caaagatgga aaattatcct tacaagtttc tccaccatta 360
aacatattaa aatcaacccat tctgaacaca ttagctgtag cttatggatc aggttttagga 420
ctcagtgggtg gcactgctct tgcagtacag ttggcctctc cactcacctt tgatgaaaaa 480
ggaaatatta aaattaacct agccagtggc ccattaacag ttgatgcaag tcgacttagt 540
atcaactgca aaagaggggt cactgtcact accgcaggag atgcaattaa aagcaacata 600
agctggccta aaggtataag atttgaaggt gatgccatag ctgcaaacat tggcagagga 660
ttggaatttg gaaccactag tacagagact gatgtcacag atgcataccc aattcaagtt 720
aaattgggta ctggtctcac ctttgacagt acaggcgcca ttggtgcatg gaacaaagag 780
gatgataaac ttacattatg gaccacagcc gaccctcgc caaattgcaa aatatactct 840
gaaaaagatg ctaaactcac actttgcttg acaaaatgtg gaagccaaat tctgggcact 900
gtgactgtat tggcagtga taatggaagt ctcaacccaa tcacaaacac agtaagcact 960
gcacttgctt ccctcaagtt tgatgcaagt ggagttttgc taagcagctc cacattagac 1020
aaagaatat t ggaacttccg aaaggagat gttacacctg ctgaacccta tactaatgct 1080
ataggtttta tgcctaacat aaaggcctat cctaaaaaca catctgcagc ttcaaaaagc 1140
catattgtca gtcaagttta tctcaatggg gatgaaacca aacctctgat gctgattatt 1200
acttttaatg aaactgagga tgcaacttgc acctatagta tcacttttca atggaaatgg 1260
gatagtacta agtacacagg taaaacactt gctaccagct ccttcacctt ctcctacatt 1320
gctcaagaat ga 1332

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&lt;210&gt; 73

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 38 Fiber

&lt;400&gt; 73

```

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
1          5          10          15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
20          25          30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
35          40          45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
50          55          60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65          70          75          80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
85          90          95
Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Thr Lys Asp Gly Lys Leu
100         105         110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Lys Ser Thr Ile Leu
115         120         125
Asn Thr Leu Ala Val Ala Tyr Gly Ser Gly Leu Gly Leu Ser Gly Gly
130         135         140
Thr Ala Leu Ala Val Gln Leu Ala Ser Pro Leu Thr Phe Asp Glu Lys
145         150         155         160

```

Gly Asn Ile Lys Ile Asn Leu Ala Ser Gly Pro Leu Thr Val Asp Ala  
 165 170 175  
 Ser Arg Leu Ser Ile Asn Cys Lys Arg Gly Val Thr Val Thr Thr Ala  
 180 185 190  
 Gly Asp Ala Ile Lys Ser Asn Ile Ser Trp Pro Lys Gly Ile Arg Phe  
 195 200 205  
 Glu Gly Asp Ala Ile Ala Ala Asn Ile Gly Arg Gly Leu Glu Phe Gly  
 210 215 220  
 Thr Thr Ser Thr Glu Thr Asp Val Thr Asp Ala Tyr Pro Ile Gln Val  
 225 230 235 240  
 Lys Leu Gly Thr Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile Val Ala  
 245 250 255  
 Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala Asp Pro  
 260 265 270  
 Ser Pro Asn Cys Lys Ile Tyr Ser Glu Lys Asp Ala Lys Leu Thr Leu  
 275 280 285  
 Cys Leu Thr Lys Cys Gly Ser Leu Asn Pro Ile Thr Asn Thr Val Ser Thr  
 290 295 300  
 Ala Val Asn Asn Gly Ser Leu Asn Pro Ile Thr Asn Thr Val Ser Thr  
 305 310 315 320  
 Ala Leu Val Ser Leu Lys Phe Asp Ala Ser Gly Val Leu Leu Ser Ser  
 325 330 335  
 Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp Val Thr  
 340 345 350  
 Pro Ala Glu Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn Ile Lys  
 355 360 365  
 Ala Tyr Pro Lys Asn Thr Ser Ala Ala Ser Lys Ser His Ile Val Ser  
 370 375 380  
 Gln Val Tyr Leu Asn Gly Asp Glu Thr Lys Pro Leu Met Leu Ile Ile  
 385 390 395 400  
 Thr Phe Asn Glu Thr Glu Asp Ala Thr Cys Thr Tyr Ser Ile Thr Phe  
 405 410 415  
 Gln Trp Lys Trp Asp Ser Thr Lys Tyr Thr Gly Lys Thr Leu Ala Thr  
 420 425 430  
 Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  
 435 440

&lt;210&gt; 74

&lt;211&gt; 1332

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 44 Fiber

&lt;400&gt; 74

atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60  
 gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120  
 gagaagcccc tgggggtgtt gtccctgcga ctggctgacc ccgtcaccac caagaacggg 180  
 gaaatcacc tcaagctggg agagggggtg gacctcgact cgctcgggaaa actcatctcc 240  
 aacacggcca ccaaggccgc cgcccctctc agtatttcaa acaacaccat ttcccttaaa 300  
 actgctgccc ctttctacaa caacaatgga actttaagcc tcaatgtctc cacaccatta 360  
 gcagtatttc ccacatttaa cacttttaggc ataagtcttg gaaacgggtc tcagacttca 420  
 aataagttgt tgactgtaca actaactcat cctcttacat tcagctcaaa tagcatcaca 480  
 gtaaaaacag acaaagggtc atatattaac tccagtggaa acagaggact tgaggcta 540  
 ataagcctaa aaagaggact agtttttgac ggtaatgcta ttgcaacata tattggaaat 600  
 ggcttagact atggatctta tgatagtgat ggaaaaacaa gaccgtaatt taccaaaatt 660  
 ggagcaggat taaattttga tgctaacaaa gcaatagctg tcaaactagg cacaggttta 720

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agttttgact cgcgtggtgc cttgacagct ggaaacaaac aggatgacaa gctaacactt 780
tggactaccc ctgacccaag ccctaattgt caattacttt cagacagaga tgccaaattt 840
actctctgtc ttacaaaatg cggtagtcaa atactaggca ctgtggcagt ggcggctgtt 900
actgtaggat cagcactaaa tccaattaat gacacagtca aaagcgccat agttttcctt 960
agatttgatt ccgatggtgt actcatgtca aactcatcaa tggtaggtga ttactggaac 1020
tttagggagg gacagaccac tcaaagtgtg gcctatacaa atgctgtggg attcatgcca 1080
aatataggtg catatccaaa aacccaaagt aaaacaccta aaaatagcat agtcagtcag 1140
gtatatatta ctggagaaac tactatgcca atgacactaa ccataacttt caatggcact 1200
gatgaaaaag acacaacccc agtttagcacc tactctatga cttttacatg gcagtggact 1260
ggagactata aggacaaaaa tattaccttt gctaccaact cattctcttt ttcctacatc 1320
gcccggaat aa 1332

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&lt;210&gt; 75

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 44 Fiber

&lt;400&gt; 75

```

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
1      5      10      15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
20      25      30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
35      40      45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
50      55      60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65      70      75      80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Ile Ser Asn Asn Thr
85      90      95
Ile Ser Leu Lys Thr Ala Ala Pro Phe Tyr Asn Asn Asn Gly Thr Leu
100     105     110
Ser Leu Asn Val Ser Thr Pro Leu Ala Val Phe Pro Thr Phe Asn Thr
115     120     125
Leu Gly Ile Ser Leu Gly Asn Gly Leu Gln Thr Ser Asn Lys Leu Leu
130     135     140
Thr Val Gln Leu Thr His Pro Leu Thr Phe Ser Ser Asn Ser Ile Thr
145     150     155     160
Val Lys Thr Asp Lys Gly Leu Tyr Ile Asn Ser Ser Gly Asn Arg Gly
165     170     175
Leu Glu Ala Asn Ile Ser Leu Lys Arg Gly Leu Val Phe Asp Gly Asn
180     185     190
Ala Ile Ala Thr Tyr Ile Gly Asn Gly Leu Asp Tyr Gly Ser Tyr Asp
195     200     205
Ser Asp Gly Lys Thr Arg Pro Val Ile Thr Lys Ile Gly Ala Gly Leu
210     215     220
Asn Phe Asp Ala Asn Lys Ala Ile Ala Val Lys Leu Gly Thr Gly Leu
225     230     235     240
Ser Phe Asp Ser Ala Gly Ala Leu Thr Ala Gly Asn Lys Gln Asp Asp
245     250     255
Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Gln Leu
260     265     270
Leu Ser Asp Arg Asp Ala Lys Phe Thr Leu Cys Leu Thr Lys Cys Gly
275     280     285

```

Ser Gln Ile Leu Gly Thr Val Ala Val Ala Ala Val Thr Val Gly Ser  
 290 295 300  
 Ala Leu Asn Pro Ile Asn Asp Thr Val Lys Ser Ala Ile Val Phe Leu  
 305 310 315 320  
 Arg Phe Asp Ser Asp Gly Val Leu Met Ser Asn Ser Ser Met Val Gly  
 325 330 335  
 Asp Tyr Trp Asn Phe Arg Glu Gly Gln Thr Thr Gln Ser Val Ala Tyr  
 340 345 350  
 Thr Asn Ala Val Gly Phe Met Pro Asn Ile Gly Ala Tyr Pro Lys Thr  
 355 360 365  
 Gln Ser Lys Thr Pro Lys Asn Ser Ile Val Ser Gln Val Tyr Leu Thr  
 370 375 380  
 Gly Glu Thr Thr Met Pro Met Thr Leu Thr Ile Thr Phe Asn Gly Thr  
 385 390 395 400  
 Asp Glu Lys Asp Thr Thr Pro Val Ser Thr Tyr Ser Met Thr Phe Thr  
 405 410 415  
 Trp Gln Trp Thr Gly Asp Tyr Lys Asp Lys Asn Ile Thr Phe Ala Thr  
 420 425 430  
 Asn Ser Phe Ser Phe Ser Tyr Ile Ala Gln Glu  
 435 440

&lt;210&gt; 76

&lt;211&gt; 1278

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 63 Fiber

&lt;400&gt; 76

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atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtgct gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgccccctctc agtttttcca acaacaccat ttcccttaac 300
atggatcacc cctttttacac taaagatgga aaattatcct tacaagtttc tccaccatta 360
aatatactga gaacaagcat tctaaacaca ctagcttttag gttttggatc aggttttagga 420
ctccgtggct ctgccttggc agtacagtta gtctctccac ttacatttga tactgatgga 480
aacataaagc ttaccttaga cagaggtttg catgtttaca caggagatgc aattgaaagc 540
aacataagct gggctaaaagg tttaaaattt gaagatggag ccatagcaac caacattgga 600
aatgggttag agtttggaag cagtagtaca gaaacagggtg ttgatgatgc ttacccaatc 660
caagttaaac ttggatctgg ccttagcttt gacagtacag gagccataat ggctggtaac 720
aaagaagacg ataaactcac tttgtggaca acacctgatc catcgccaaa ctgtcaaata 780
ctcgcagaaa atgatgcaaa actaacactt tgcttgacta aatgtggtag tcaaatactg 840
gccactgtgt cagtcttagt tgttaggaagt ggaaacctaa accccattac tggcaccgta 900
agcagtgtct aggtgtttct acgttttgat gcaaacgggtg ttcttttaac agaacattct 960
acactaaaaa aatactgggg gtataggcag ggagatagca tagatggcac tccatatacc 1020
aatgctgtag gattcatgcc caatttaaaa gcttatccaa agtcacaaag ttctactact 1080
aaaaataata tagtagggca agtatacatg aatggagatg tttcaaaacc tatgctttctc 1140
actataaccc tcaatggtac tgatgacagc aacagtacat attcaatgtc attttcatac 1200
acctggacta atggaagcta tgttgaggca acatttgggg ctaactctta taccttctca 1260
tacatcgccc aagaatga
1278

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&lt;210&gt; 77

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 63 Fiber

&lt;400&gt; 77

Met	Ser	Lys	Lys	Arg	Val	Arg	Val	Asp	Asp	Asp	Phe	Asp	Pro	Val	Tyr
1				5					10					15	
Pro	Tyr	Asp	Ala	Asp	Asn	Ala	Pro	Thr	Val	Pro	Phe	Ile	Asn	Pro	Pro
			20					25					30		
Phe	Val	Ser	Ser	Asp	Gly	Phe	Gln	Glu	Lys	Pro	Leu	Gly	Val	Leu	Ser
		35					40					45			
Leu	Arg	Leu	Ala	Asp	Pro	Val	Thr	Thr	Lys	Asn	Gly	Glu	Ile	Thr	Leu
50						55					60				
Lys	Leu	Gly	Glu	Gly	Val	Asp	Leu	Asp	Ser	Ser	Gly	Lys	Leu	Ile	Ser
65					70					75					80
Asn	Thr	Ala	Thr	Lys	Ala	Ala	Ala	Pro	Leu	Ser	Phe	Ser	Asn	Asn	Thr
				85					90					95	
Ile	Ser	Leu	Asn	Met	Asp	His	Pro	Phe	Tyr	Thr	Lys	Asp	Gly	Lys	Leu
			100					105					110		
Ser	Leu	Gln	Val	Ser	Pro	Pro	Leu	Asn	Ile	Leu	Arg	Thr	Ser	Ile	Leu
		115					120					125			
Asn	Thr	Leu	Ala	Leu	Gly	Phe	Gly	Ser	Gly	Leu	Gly	Leu	Arg	Gly	Ser
130						135					140				
Ala	Leu	Ala	Val	Gln	Leu	Val	Ser	Pro	Leu	Thr	Phe	Asp	Thr	Asp	Gly
145				150						155					160
Asn	Ile	Lys	Leu	Thr	Leu	Asp	Arg	Gly	Leu	His	Val	Thr	Thr	Gly	Asp
				165					170					175	
Ala	Ile	Glu	Ser	Asn	Ile	Ser	Trp	Ala	Lys	Gly	Leu	Lys	Phe	Glu	Asp
			180					185					190		
Gly	Ala	Ile	Ala	Thr	Asn	Ile	Gly	Asn	Gly	Leu	Glu	Phe	Gly	Ser	Ser
		195					200					205			
Ser	Thr	Glu	Thr	Gly	Val	Asp	Asp	Ala	Tyr	Pro	Ile	Gln	Val	Lys	Leu
210					215						220				
Gly	Ser	Gly	Leu	Ser	Phe	Asp	Ser	Thr	Gly	Ala	Ile	Met	Ala	Gly	Asn
225					230				235						240
Lys	Glu	Asp	Asp	Lys	Leu	Thr	Leu	Trp	Thr	Thr	Pro	Asp	Pro	Ser	Pro
			245						250					255	
Asn	Cys	Gln	Ile	Leu	Ala	Glu	Asn	Asp	Ala	Lys	Leu	Thr	Leu	Cys	Leu
			260					265					270		
Thr	Lys	Cys	Gly	Ser	Gln	Ile	Leu	Ala	Thr	Val	Ser	Val	Leu	Val	Val
		275					280					285			
Gly	Ser	Gly	Asn	Leu	Asn	Pro	Ile	Thr	Gly	Thr	Val	Ser	Ser	Ala	Gln
290					295						300				
Val	Phe	Leu	Arg	Phe	Asp	Ala	Asn	Gly	Val	Leu	Leu	Thr	Glu	His	Ser
305					310					315					320
Thr	Leu	Lys	Lys	Tyr	Trp	Gly	Tyr	Arg	Gln	Gly	Asp	Ser	Ile	Asp	Gly
				325					330					335	
Thr	Pro	Tyr	Thr	Asn	Ala	Val	Gly	Phe	Met	Pro	Asn	Leu	Lys	Ala	Tyr
			340					345					350		
Pro	Lys	Ser	Gln	Ser	Ser	Thr	Thr	Lys	Asn	Asn	Ile	Val	Gly	Gln	Val
		355					360					365			
Tyr	Met	Asn	Gly	Asp	Val	Ser	Lys	Pro	Met	Leu	Leu	Thr	Ile	Thr	Leu
370					375						380				
Asn	Gly	Thr	Asp	Asp	Ser	Asn	Ser	Thr	Tyr	Ser	Met	Ser	Phe	Ser	Tyr
385					390					395					400
Thr	Trp	Thr	Asn	Gly	Ser	Tyr	Val	Gly	Ala	Thr	Phe	Gly	Ala	Asn	Ser
				405					410					415	
Tyr	Thr	Phe	Ser	Tyr	Ile	Ala	Gln	Glu							
			420					425							

<210> 78  
 <211> 1338  
 <212> DNA  
 <213> Chimpanzee Adenovirus- ChAd 82 Fiber

<400> 78  
 atgtccaaaa agcgcgcgcg ggtggatgat gacttcgacc ccgtgtaccc ctacgatgca 60  
 gacaacgcac cgactgtgcc cttcatcaac cctcccttcg tctcttcaga tggattccaa 120  
 gaaaagcccc tgggggtgtt gtccctgcga ctggccgac ccgtcaccac caagaacggg 180  
 gctgtcacc tcaagctggg ggagggggtg gacctcgacg actcgggaaa actcatctcc 240  
 aaaaatgcca ccaaggccac tgccctctc agtatttcca acaacaccat ttcccttaac 300  
 atggataccc ctctttacaa caacaatgga aagctaggta tgaaggtaac cgcaccatta 360  
 aagatattag acacagatct actaaaaaca cttgttggtt cttatgggca gggattagga 420  
 acaaacacca atggtgctct tgttgcccaa ctagcatacc cacttgtttt taataccgct 480  
 agcaaaattg cccttaattt aggcaatgga ccattaaaag tggatgcaaa tagactgaac 540  
 attaattgca aaagaggtat ctatgtcact accacaaaag atgcactgga gattaatatc 600  
 agttggggcaa atgctatgac atttatagga aatgccattg gtgtcaatat tgacacaaaa 660  
 aaaggcctac agttcggcac ttcaagcact gaaacagatg ttaaaaatgc ttttccactc 720  
 caagtaaaac ttggagctgg tcttacattt gacagcacag gtgccattgt tgcttggaac 780  
 aaagaagatg acaaacttac actgtggacc acagccgacg catctccaaa ctgtcacata 840  
 tattctgcaa aggatgctaa gcttacctc tgcttgacaa agtgtggtag tcagatactg 900  
 ggcactgttt ctctcatagc tgttgatact ggtagcttaa atccaataac agggaaagta 960  
 accactgctc ttgtttcact taaattcgat gccaatggag ttttgcaagc cagttcaaca 1020  
 ctagataaag aatattggaa tttcagaaaa ggagatgtga cacttgctga cccctacact 1080  
 aatgctatag gctttatgcc caaccttaat gcatacccaa aaaacacaaa cgcagctgca 1140  
 aaaagtcaca ttgttggaag agtataccta catggggatg taagcaagcc actagacttg 1200  
 ataattacat ttaatgaaac cagtgatgaa tcctgtactt attgcattaa ctttcagtgg 1260  
 cgggtgggaa ctgaccaata taaagatgaa acacttgcag tcagttcatt caccttctca 1320  
 tacattgcta aagaataa 1338

<210> 79  
 <211> 445  
 <212> PRT  
 <213> Chimpanzee Adenovirus- ChAd 82 Fiber

<400> 79  
 Met Ser Lys Lys Arg Ala Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Ala Val Thr Leu  
 50 55 60  
 Lys Leu Gly Glu Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Lys Asn Ala Thr Lys Ala Thr Ala Pro Leu Ser Ile Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu  
 100 105 110  
 Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu  
 115 120 125  
 Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn  
 130 135 140



Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala  
 145 150 155 160  
 Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala  
 165 170 175  
 Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr  
 180 185 190  
 Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe  
 195 200 205  
 Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln  
 210 215 220  
 Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Pro Leu  
 225 230 235 240  
 Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile  
 245 250 255  
 Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala  
 260 265 270  
 Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu  
 275 280 285  
 Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser  
 290 295 300  
 Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Lys Val  
 305 310 315 320  
 Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln  
 325 330 335  
 Ala Ser Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp  
 340 345 350  
 Val Thr Pro Ala Asp Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn  
 355 360 365  
 Leu Asn Ala Tyr Pro Lys Asn Thr Asn Ala Ala Ala Lys Ser His Ile  
 370 375 380  
 Val Gly Lys Val Tyr Leu His Gly Asp Val Ser Lys Pro Leu Asp Leu  
 385 390 395 400  
 Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile  
 405 410 415  
 Asn Phe Gln Trp Arg Trp Gly Thr Asp Gln Tyr Lys Asp Glu Thr Leu  
 420 425 430  
 Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu  
 435 440 445

&lt;210&gt; 80

&lt;211&gt; 445

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV23/Pan5 Fiber

&lt;400&gt; 80

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
 1 5 10 15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60  
 Lys Leu Gly Asp Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65 70 75 80

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Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
      85      90      95
Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Asn Asn Asn Gly Lys Leu
      100      105      110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
      115      120      125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Thr
      130      135      140
Gly Ala Leu Val Ala Gln Leu Ala Ser Pro Leu Ala Phe Asp Ser Asn
145      150      155      160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
      165      170      175
Asn Arg Leu Asn Ile Asn Cys Asn Arg Gly Leu Tyr Val Thr Thr Thr
      180      185      190
Lys Asp Ala Leu Glu Ala Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
      195      200      205
Ile Gly Asn Ala Met Gly Val Asn Ile Asp Thr Gln Lys Gly Leu Gln
      210      215      220
Phe Gly Thr Thr Ser Thr Val Ala Asp Val Lys Asn Ala Tyr Pro Ile
225      230      235      240
Gln Ile Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
      245      250      255
Val Ala Trp Asn Lys Asp Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
      260      265      270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Glu Lys Asp Ala Lys Leu
      275      280      285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
      290      295      300
Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Thr Val
305      310      315      320
Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln
      325      330      335
Ser Ser Ser Thr Leu Asp Ser Asp Tyr Trp Asn Phe Arg Gln Gly Asp
      340      345      350
Val Thr Pro Ala Glu Ala Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn
      355      360      365
Leu Lys Ala Tyr Pro Lys Asn Thr Ser Gly Ala Ala Lys Ser His Ile
      370      375      380
Val Gly Lys Val Tyr Leu His Gly Asp Thr Gly Lys Pro Leu Asp Leu
385      390      395      400
Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile
      405      410      415
Asn Phe Gln Trp Gln Trp Gly Ala Asp Gln Tyr Lys Asn Glu Thr Leu
      420      425      430
Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu
      435      440      445

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&lt;210&gt; 81

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV32/Pan6 Fiber

&lt;400&gt; 81

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Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1              5              10              15

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Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
 20 25 30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
 35 40 45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
 50 55 60  
 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65 70 75 80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Ile Ser Asn Asn Thr  
 85 90 95  
 Ile Ser Leu Lys Thr Ala Ala Pro Phe Tyr Asn Asn Asn Gly Thr Leu  
 100 105 110  
 Ser Leu Asn Val Ser Thr Pro Leu Ala Val Phe Pro Thr Phe Asn Thr  
 115 120 125  
 Leu Gly Ile Ser Leu Gly Asn Gly Leu Gln Thr Ser Asn Lys Leu Leu  
 130 135 140  
 Thr Val Gln Leu Thr His Pro Leu Thr Phe Ser Ser Asn Ser Ile Thr  
 145 150 155 160  
 Val Lys Thr Asp Lys Gly Leu Tyr Ile Asn Ser Ser Gly Asn Arg Gly  
 165 170 175  
 Leu Glu Ala Asn Ile Ser Leu Lys Arg Gly Leu Val Phe Asp Gly Asn  
 180 185 190  
 Ala Ile Ala Thr Tyr Ile Gly Asn Gly Leu Asp Tyr Gly Ser Tyr Asp  
 195 200 205  
 Ser Asp Gly Lys Thr Arg Pro Val Ile Thr Lys Ile Gly Ala Gly Leu  
 210 215 220  
 Asn Phe Asp Ala Asn Lys Ala Ile Ala Val Lys Leu Gly Thr Gly Leu  
 225 230 235 240  
 Ser Phe Asp Ser Ala Gly Ala Leu Thr Ala Gly Asn Lys Gln Asp Asp  
 245 250 255  
 Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Gln Leu  
 260 265 270  
 Leu Ser Asp Arg Asp Ala Lys Phe Thr Leu Cys Leu Thr Lys Cys Gly  
 275 280 285  
 Ser Gln Ile Leu Gly Thr Val Ala Val Ala Ala Val Thr Val Gly Ser  
 290 295 300  
 Ala Leu Asn Pro Ile Asn Asp Thr Val Lys Ser Ala Ile Val Phe Leu  
 305 310 315 320  
 Arg Phe Asp Ser Asp Gly Val Leu Met Ser Asn Ser Ser Met Val Gly  
 325 330 335  
 Asp Tyr Trp Asn Phe Arg Glu Gly Gln Thr Thr Gln Ser Val Ala Tyr  
 340 345 350  
 Thr Asn Ala Val Gly Phe Met Pro Asn Ile Gly Ala Tyr Pro Lys Thr  
 355 360 365  
 Gln Ser Lys Thr Pro Lys Asn Ser Ile Val Ser Gln Val Tyr Leu Thr  
 370 375 380  
 Gly Glu Thr Thr Met Pro Met Thr Leu Thr Ile Thr Phe Asn Gly Thr  
 385 390 395 400  
 Asp Glu Lys Asp Thr Thr Pro Val Ser Thr Tyr Ser Met Thr Phe Thr  
 405 410 415  
 Trp Gln Trp Thr Gly Asp Tyr Lys Asp Lys Asn Ile Thr Phe Ala Thr  
 420 425 430  
 Asn Ser Phe Ser Phe Ser Tyr Ile Ala Gln Glu  
 435 440

&lt;210&gt; 82

&lt;211&gt; 443

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV33/Pan7 Fiber

&lt;400&gt; 82

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Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
1      5      10      15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
20      25      30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
35      40      45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
50      55      60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65      70      75      80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
85      90      95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Thr Lys Asp Gly Lys Leu
100      105      110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Lys Ser Thr Ile Leu
115      120      125
Asn Thr Leu Ala Val Ala Tyr Gly Ser Gly Leu Gly Leu Ser Gly Gly
130      135      140
Thr Ala Leu Ala Val Gln Leu Ala Ser Pro Leu Thr Phe Asp Glu Lys
145      150      155      160
Gly Asn Ile Lys Ile Asn Leu Ala Ser Gly Pro Leu Thr Val Asp Ala
165      170      175
Ser Arg Leu Ser Ile Asn Cys Lys Arg Gly Val Thr Val Thr Thr Ser
180      185      190
Gly Asp Ala Ile Glu Ser Asn Ile Ser Trp Pro Lys Gly Ile Arg Phe
195      200      205
Glu Gly Asn Gly Ile Ala Ala Asn Ile Gly Arg Gly Leu Glu Phe Gly
210      215      220
Thr Thr Ser Thr Glu Thr Asp Val Thr Asp Ala Tyr Pro Ile Gln Val
225      230      235      240
Lys Leu Gly Thr Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile Val Ala
245      250      255
Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala Asp Pro
260      265      270
Ser Pro Asn Cys Lys Ile Tyr Ser Glu Lys Asp Ala Lys Leu Thr Leu
275      280      285
Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Thr Val Leu
290      295      300
Ala Val Asn Asn Gly Ser Leu Asn Pro Ile Thr Asn Thr Val Ser Thr
305      310      315      320
Ala Leu Val Ser Leu Lys Phe Asp Ala Ser Gly Val Leu Leu Ser Ser
325      330      335
Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp Val Thr
340      345      350
Pro Ala Glu Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn Ile Lys
355      360      365
Ala Tyr Pro Lys Asn Thr Ser Ala Ala Ser Lys Ser His Ile Val Ser
370      375      380

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Gln Val Tyr Leu Asn Gly Asp Glu Ala Lys Pro Leu Met Leu Ile Ile  
 385 390 395 400  
 Thr Phe Asn Glu Thr Glu Asp Ala Thr Cys Thr Tyr Ser Ile Thr Phe  
 405 410 415  
 Gln Trp Lys Trp Asp Ser Thr Lys Tyr Thr Gly Glu Thr Leu Ala Thr  
 420 425 430  
 Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu  
 435 440

&lt;210&gt; 83

&lt;211&gt; 543

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 3 Fiber

&lt;400&gt; 83

Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro  
 1 5 10 15  
 Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro  
 20 25 30  
 Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser  
 35 40 45  
 Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu  
 50 55 60  
 Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser  
 65 70 75 80  
 Gln Asp Ile Thr Thr Ala Ser Pro Pro Leu Lys Lys Thr Lys Thr Asn  
 85 90 95  
 Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala  
 100 105 110  
 Leu Thr Val Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu  
 115 120 125  
 Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr  
 130 135 140  
 Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu  
 145 150 155 160  
 Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val  
 165 170 175  
 Ser Ala Thr Pro Pro Ile Asn Val Ser Ser Gly Ser Leu Gly Leu Asp  
 180 185 190  
 Met Glu Asp Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile  
 195 200 205  
 Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val  
 210 215 220  
 Thr Gly Asn Gly Leu Thr Val Asp Asn Asn Ala Leu Gln Thr Arg Val  
 225 230 235 240  
 Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala  
 245 250 255  
 Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asn Val  
 260 265 270  
 Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln  
 275 280 285  
 Gly Pro Leu Tyr Ile Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn  
 290 295 300  
 Arg Gly Leu Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr  
 305 310 315 320

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<210> 84
<211> 445
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 6 Fiber
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Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
      165      170      175
Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr
      180      185      190
Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
      195      200      205
Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln
      210      215      220
Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Pro Leu
      225      230      235      240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
      245      250      255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
      260      265      270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu
      275      280      285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
      290      295      300
Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Lys Val
      305      310      315      320
Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln
      325      330      335
Ala Ser Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp
      340      345      350
Val Thr Pro Ala Asp Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn
      355      360      365
Leu Asn Ala Tyr Pro Lys Asn Thr Asn Ala Ala Ala Lys Ser His Ile
      370      375      380
Val Gly Lys Val Tyr Leu His Gly Asp Glu Ser Lys Pro Leu Asp Leu
      385      390      395      400
Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile
      405      410      415
Asn Phe Gln Trp Gln Trp Gly Thr Asp Gln Tyr Lys Asp Glu Thr Leu
      420      425      430
Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu
      435      440      445

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&lt;210&gt; 85

&lt;211&gt; 322

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- C1 Fiber

&lt;400&gt; 85

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Met Ala Lys Arg Thr Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
  1      5      10      15
Tyr Glu Asp Glu Asn Ser Ser His Pro Phe Ile Asn Pro Gly Phe Ile
      20      25      30
Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Asn
      35      40      45
Cys Val Ala Pro Leu Thr Thr Ala Asn Gly Ala Leu Asp Ile Lys Val
      50      55      60
Gly Gly Gly Leu Lys Val Asn Ser Thr Asp Gly Phe Leu Glu Glu Asn
      65      70      75      80
Ile Asn Ile Thr Ser Pro Leu Thr Lys Ser Asn His Ser Ile Gly Leu
      85      90      95

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Glu Trp Ser Asp Gly Leu Gln Thr Asn Glu Ala Lys Leu Cys Val Lys  
                           100                          105                          110  
 Leu Gly Lys Gly Leu Val Phe Asp Ser Ser Ser Ala Ile Ala Met Glu  
                           115                          120                          125  
 Asn Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile  
                           130                          135                          140  
 Lys Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val  
 145                          150                          155                          160  
 Lys Asn Gly Gly Leu Val Asn Gly Tyr Ile Thr Leu Met Gly Asp Ser  
                           165                          170                          175  
 Glu Tyr Thr Asn Thr Leu Phe Lys Asn Lys Gln Val Thr Ile Asp Val  
                           180                          185                          190  
 Asn Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser  
                           195                          200                          205  
 Leu Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly  
                           210                          215                          220  
 Thr Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro  
 225                          230                          235                          240  
 Phe Ile Thr Tyr Ala Thr Gln Ser Leu Asn Glu Asp Tyr Ile Tyr Gly  
                           245                          250                          255  
 Glu Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val  
                           260                          265                          270  
 Thr Val Thr Leu Asn Arg Arg Met Ser Ala Ser Gly Met Ala Tyr Ala  
                           275                          280                          285  
 Met Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr  
                           290                          295                          300  
 Glu Val Thr Leu Ile Thr Ser Pro Phe Phe Phe Ser Tyr Ile Arg Glu  
 305                          310                          315                          320  
 Asp Asp

&lt;210&gt; 86

&lt;211&gt; 425

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV68 Fiber

&lt;400&gt; 86

Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr  
   1                          5                          10                          15  
 Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro  
                           20                          25                          30  
 Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser  
                           35                          40                          45  
 Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu  
                           50                          55                          60  
 Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser  
 65                          70                          75                          80  
 Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr  
                           85                          90                          95  
 Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu  
                           100                          105                          110  
 Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu  
                           115                          120                          125  
 Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser  
                           130                          135                          140



Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly  
 145 150 155 160  
 Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp  
 165 170 175  
 Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp  
 180 185 190  
 Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser  
 195 200 205  
 Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu  
 210 215 220  
 Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn  
 225 230 235 240  
 Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro  
 245 250 255  
 Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu  
 260 265 270  
 Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val  
 275 280 285  
 Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln  
 290 295 300  
 Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser  
 305 310 315 320  
 Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly  
 325 330 335  
 Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr  
 340 345 350  
 Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val  
 355 360 365  
 Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu  
 370 375 380  
 Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr  
 385 390 395 400  
 Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser  
 405 410 415  
 Tyr Thr Phe Ser Tyr Ile Ala Gln Glu  
 420 425

&lt;210&gt; 87

&lt;211&gt; 954

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd20 Hexon

&lt;400&gt; 87

Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr  
 65 70 75 80  
 Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95

Ala	Ser	Thr	Tyr	Phe	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Pro	Thr	
			100					105					110			
Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly	
		115					120					125				
Ala	Pro	Asn	Pro	Cys	Glu	Trp	Asp	Glu	Ala	Ala	Thr	Ala	Leu	Asp	Ile	
		130				135					140					
Asp	Leu	Asn	Ala	Glu	Asp	Asp	Glu	Glu	Ser	Asp	Glu	Ala	Gln	Gly	Glu	
145					150					155					160	
Ala	Asp	Gln	Gln	Lys	Thr	His	Val	Phe	Gly	Gln	Ala	Pro	Tyr	Ser	Gly	
				165					170						175	
Gln	Asn	Ile	Thr	Lys	Glu	Gly	Ile	Gln	Ile	Gly	Ile	Asp	Ala	Ala	Ser	
			180					185					190			
Gln	Ala	Gln	Thr	Pro	Val	Tyr	Ala	Asp	Lys	Thr	Phe	Gln	Pro	Glu	Pro	
		195					200					205				
Gln	Val	Gly	Glu	Ser	Gln	Trp	Asn	Glu	Thr	Glu	Ile	Ser	Tyr	Gly	Ala	
	210					215					220					
Gly	Arg	Val	Leu	Lys	Lys	Thr	Thr	Leu	Met	Lys	Pro	Cys	Tyr	Gly	Ser	
225					230					235					240	
Tyr	Ala	Arg	Pro	Thr	Asn	Glu	Asn	Gly	Gly	Gln	Gly	Ile	Leu	Leu	Glu	
				245				250							255	
Gln	Asp	Gly	Lys	Lys	Glu	Ser	Gln	Val	Glu	Met	Gln	Phe	Phe	Ser	Thr	
			260					265						270		
Thr	Gln	Ala	Ala	Ala	Gly	Asn	Ser	Asp	Asn	Pro	Thr	Pro	Lys	Val	Val	
		275					280					285				
Leu	Tyr	Ser	Glu	Asp	Val	Asn	Leu	Glu	Thr	Pro	Asp	Thr	His	Ile	Ser	
	290					295					300					
Tyr	Met	Pro	Thr	Asn	Asn	Glu	Thr	Asn	Ser	Arg	Glu	Leu	Leu	Gly	Gln	
305					310					315					320	
Gln	Ala	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe	
				325					330					335		
Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala	
			340					345						350		
Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn	
		355					360					365				
Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Met	Gly	Asp	Arg	Thr	
	370					375						380				
Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	
385					390					395					400	
Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Thr	Glu	Asp	Glu	Leu	Pro	Asn	Tyr	
				405				410						415		
Cys	Phe	Pro	Leu	Gly	Gly	Val	Ile	Asn	Thr	Glu	Thr	Phe	Thr	Lys	Val	
			420					425						430		
Lys	Pro	Lys	Ala	Ala	Gln	Asp	Ala	Gln	Trp	Glu	Lys	Asp	Ser	Glu	Phe	
		435					440					445				
Ser	Asp	Lys	Asn	Glu	Ile	Arg	Val	Gly	Asn	Asn	Phe	Ala	Met	Glu	Ile	
	450					455					460					
Asn	Leu	Asn	Ala	Asn	Leu	Trp	Arg	Asn	Phe	Leu	Tyr	Ser	Asn	Val	Ala	
465					470					475					480	
Leu	Tyr	Leu	Pro	Asp	Lys	Leu	Lys	Tyr	Thr	Pro	Ser	Asn	Val	Gln	Ile	
				485				490						495		
Ser	Asn	Asn	Pro	Asn	Ser	Tyr	Asp	Tyr	Met	Asn	Lys	Arg	Val	Val	Ala	
			500					505						510		
Pro	Gly	Leu	Val	Asp	Cys	Tyr	Ile	Asn	Leu	Gly	Ala	Arg	Trp	Ser	Leu	
		515					520					525				

Asp	Tyr	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn	Ala	Gly
530						535					540				
Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe
545					550					555					560
His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys	Asn	Leu	Leu	Leu
				565					570						575
Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn
			580					585					590		
Met	Val	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Val	Asp	Gly	Ala
		595					600					605			
Ser	Ile	Lys	Phe	Glu	Ser	Ile	Cys	Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met
610						615					620				
Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr
625					630					635					640
Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr
				645					650						655
Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	Pro	Ser	Arg
			660					665					670		
Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ala	Phe	Thr	Arg	Leu	Lys	Thr	Lys
		675					680					685			
Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Tyr	Thr	Tyr	Ser
690						695					700				
Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe
705					710					715					720
Lys	Lys	Val	Ser	Val	Thr	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn
				725					730						735
Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	Ser	Val	Asp
			740					745					750		
Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe
		755					760					765			
Leu	Val	Gln	Met	Leu	Ala	Asn	Tyr	Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr
770						775					780				
Ile	Pro	Glu	Ser	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe
785					790					795					800
Gln	Pro	Met	Ser	Arg	Gln	Val	Val	Asp	Gln	Thr	Lys	Tyr	Lys	Asp	Tyr
				805					810					815	
Gln	Glu	Val	Gly	Ile	Ile	His	Gln	His	Asn	Asn	Ser	Gly	Phe	Val	Gly
			820					825					830		
Tyr	Leu	Ala	Pro	Thr	Met	Arg	Glu	Gly	Gln	Ala	Tyr	Pro	Ala	Asn	Phe
		835					840					845			
Pro	Tyr	Pro	Leu	Ile	Gly	Lys	Thr	Ala	Val	Asp	Ser	Ile	Thr	Gln	Lys
		850				855					860				
Lys	Phe	Leu	Cys	Asp	Arg	Thr	Leu	Trp	Arg	Ile	Pro	Phe	Ser	Ser	Asn
865					870					875					880
Phe	Met	Ser	Met	Gly	Ala	Leu	Ser	Asp	Leu	Gly	Gln	Asn	Leu	Leu	Tyr
				885					890					895	
Ala	Asn	Ser	Ala	His	Ala	Leu	Asp	Met	Thr	Phe	Glu	Val	Asp	Pro	Met
			900					905					910		
Asp	Glu	Pro	Thr	Leu	Leu	Tyr	Val	Leu	Phe	Glu	Val	Phe	Asp	Val	Val
		915					920					925			
Arg	Val	His	Gln	Pro	His	Arg	Gly	Val	Ile	Glu	Thr	Val	Tyr	Leu	Arg
930						935					940				

Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
945 950

<210> 88

<211> 940

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 4 Hexon

<400> 88

Met	Ala	Thr	Pro	Ser	Met	Leu	Pro	Gln	Trp	Ala	Tyr	Met	His	Ile	Ala
1				5					10					15	
Gly	Gln	Asp	Ala	Ser	Glu	Tyr	Leu	Ser	Pro	Gly	Leu	Val	Gln	Phe	Ala
		20						25					30		
Arg	Ala	Thr	Asp	Thr	Tyr	Phe	Ser	Leu	Gly	Asn	Lys	Phe	Arg	Asn	Pro
		35					40					45			
Thr	Val	Ala	Pro	Thr	His	Asp	Val	Thr	Thr	Asp	Arg	Ser	Gln	Arg	Leu
	50				55						60				
Thr	Leu	Arg	Phe	Val	Pro	Val	Asp	Arg	Glu	Asp	Asn	Thr	Tyr	Ser	Tyr
65				70					75						80
Lys	Val	Arg	Tyr	Thr	Leu	Ala	Val	Gly	Asp	Asn	Arg	Val	Leu	Asp	Met
			85					90					95		
Ala	Ser	Thr	Tyr	Phe	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Pro	Ser
		100						105					110		
Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly
	115					120					125				
Ala	Pro	Asn	Ser	Ser	Gln	Trp	Glu	Gln	Lys	Lys	Thr	Gly	Asn	Asn	Ala
	130				135						140				
Asn	Gly	Asp	Thr	Glu	Asn	Val	Thr	Tyr	Gly	Val	Ala	Ala	Met	Gly	Gly
145				150						155					160
Ile	Asp	Ile	Asp	Lys	Asn	Gly	Leu	Gln	Ile	Gly	Thr	Asp	Asp	Thr	Lys
			165					170						175	
Asp	Asp	Asp	Asn	Glu	Ile	Tyr	Ala	Asp	Lys	Thr	Tyr	Gln	Pro	Glu	Pro
			180					185					190		
Gln	Ile	Gly	Glu	Glu	Asn	Trp	Gln	Glu	Thr	Tyr	Ser	Tyr	Tyr	Gly	Gly
	195					200						205			
Arg	Ala	Leu	Lys	Lys	Asp	Thr	Lys	Met	Lys	Pro	Cys	Tyr	Gly	Ser	Phe
	210				215						220				
Ala	Arg	Pro	Thr	Asn	Val	Lys	Gly	Gly	Gln	Ala	Lys	Ile	Lys	Thr	Asp
225				230						235					240
Gly	Asp	Val	Lys	Ser	Phe	Asp	Ile	Asp	Leu	Ala	Phe	Phe	Asp	Ile	Pro
			245					250						255	
Asn	Ser	Gly	Ala	Gly	Asn	Gly	Thr	Asn	Val	Asn	Asp	Asp	Pro	Asp	Met
		260					265						270		
Val	Met	Tyr	Thr	Glu	Asn	Val	Asn	Leu	Glu	Thr	Pro	Asp	Thr	His	Ile
	275					280						285			
Val	Tyr	Lys	Pro	Gly	Thr	Ser	Asp	Asp	Ser	Ser	Lys	Val	Asn	Leu	Cys
	290				295						300				
Gln	Gln	Ser	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn
305				310						315					320
Phe	Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu
			325					330					335		
Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg
		340					345						350		
Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly	Asp	Arg
	355						360						365		

Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro
	370					375					380				
Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu	Pro	Asn
385					390					395					400
Tyr	Cys	Phe	Pro	Leu	Asp	Gly	Ala	Gly	Thr	Asn	Ser	Val	Tyr	Gln	Gly
				405					410					415	
Val	Lys	Pro	Lys	Thr	Asp	Asn	Gly	Asn	Asp	Gln	Trp	Glu	Thr	Asp	Ser
			420					425					430		
Thr	Val	Ser	Ser	His	Asn	Gln	Ile	Cys	Lys	Gly	Asn	Ile	Tyr	Ala	Met
		435					440					445			
Glu	Ile	Asn	Leu	Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr	Ser	Asn
	450					455					460				
Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	Ile
465					470					475					480
Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Gly	Arg	Val
				485					490					495	
Val	Pro	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Ile	Asn	Ile	Gly	Ala	Arg	Trp
			500					505					510		
Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn
		515					520					525			
Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val
	530					535					540				
Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys	Ser	Leu
545					550					555					560
Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp
				565					570					575	
Val	Asn	Met	Ile	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Thr	Asp
			580					585					590		
Gly	Ala	Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	Phe
		595					600					605			
Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn
	610					615					620				
Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met
625					630					635					640
Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	Pro
				645					650					655	
Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	Lys
			660					665					670		
Thr	Arg	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Phe	Val
		675					680					685			
Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His
	690					695					700				
Thr	Phe	Lys	Lys	Val	Ser	Ile	Thr	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro
705					710					715					720
Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	Thr
				725					730					735	
Val	Asp	Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	Asp
			740					745					750		
Trp	Phe	Leu	Val	Gln	Met	Leu	Ala	His	Tyr	Asn	Ile	Gly	Tyr	Gln	Gly
		755					760					765			
Phe	Tyr	Val	Pro	Glu	Gly	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	Arg
	770					775					780				
Asn	Phe	Gln	Pro	Met	Ser	Arg	Gln	Val	Val	Asp	Glu	Val	Asn	Tyr	Lys
785					790					795					800

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Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe
      805      810      815
Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala
      820      825      830
Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr
      835      840      845
Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser
      850      855      860
Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met
865      870      875      880
Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp
      885      890      895
Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp
      900      905      910
Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr
      915      920      925
Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
      930      935      940

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&lt;210&gt; 89

&lt;211&gt; 940

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 5 Hexon

&lt;400&gt; 89

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
  1      5      10      15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
      20      25      30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
      35      40      45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
      50      55      60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65      70      75      80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
      85      90      95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
      100      105      110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
      115      120      125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Lys Lys Thr Gly Asn Asn Ala
      130      135      140
Asn Gly Asp Thr Glu Asn Val Thr Tyr Gly Val Ala Ala Met Gly Gly
145      150      155      160
Ile Asp Ile Asp Lys Asn Gly Leu Gln Ile Gly Thr Asp Asp Thr Lys
      165      170      175
Asp Asp Asp Asn Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro
      180      185      190
Gln Ile Gly Glu Glu Asn Trp Gln Glu Thr Tyr Ser Tyr Tyr Gly Gly
      195      200      205
Arg Ala Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe
      210      215      220
Ala Arg Pro Thr Asn Val Lys Gly Gly Gln Ala Lys Ile Lys Thr Asp
225      230      235      240

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Gly Asp Val Lys Ser Phe Asp Ile Asp Leu Ala Phe Phe Asp Ile Pro  
 245 250 255  
 Asn Ser Gly Ala Gly Asn Gly Thr Asn Val Asn Asp Asp Pro Asp Met  
 260 265 270  
 Val Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile  
 275 280 285  
 Val Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Lys Val Asn Leu Cys  
 290 295 300  
 Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn  
 305 310 315 320  
 Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu  
 325 330 335  
 Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg  
 340 345 350  
 Asn Thr Glu Leu Ser Tyr Gln Leu Leu Asp Ser Leu Gly Asp Arg  
 355 360 365  
 Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro  
 370 375 380  
 Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn  
 385 390 395 400  
 Tyr Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ser Val Tyr Gln Gly  
 405 410 415  
 Val Lys Pro Lys Thr Asp Asn Gly Asn Asp Gln Trp Glu Thr Asp Ser  
 420 425 430  
 Thr Val Ser Ser His Asn Gln Ile Cys Lys Gly Asn Ile Tyr Ala Met  
 435 440 445  
 Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn  
 450 455 460  
 Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile  
 465 470 475 480  
 Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val  
 485 490 495  
 Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp  
 500 505 510  
 Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn  
 515 520 525  
 Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val  
 530 535 540  
 Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu  
 545 550 555 560  
 Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp  
 565 570 575  
 Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp  
 580 585 590  
 Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe  
 595 600 605  
 Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn  
 610 615 620  
 Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met  
 625 630 635 640  
 Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro  
 645 650 655  
 Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys  
 660 665 670

Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val  
 675 680 685  
 Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His  
 690 695 700  
 Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro  
 705 710 715 720  
 Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr  
 725 730 735  
 Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp  
 740 745 750  
 Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly  
 755 760 765  
 Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg  
 770 775 780  
 Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys  
 785 790 795 800  
 Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe  
 805 810 815  
 Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala  
 820 825 830  
 Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser Val Thr  
 835 840 845  
 Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser  
 850 855 860  
 Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met  
 865 870 875 880  
 Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp  
 885 890 895  
 Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp  
 900 905 910  
 Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr  
 915 920 925  
 Leu Arg Thr Pro Phe Ser Ala Gly Lys Ala Thr Thr  
 930 935 940

&lt;210&gt; 90

&lt;211&gt; 940

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 7 Hexon

&lt;400&gt; 90

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
 65 70 75 80  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
 100 105 110



Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Ser Ser Gln Trp Glu Gln Lys Lys Thr Gly Lys Asn Ala  
 130 135 140  
 Asn Gly Asp Thr Glu Asn Val Thr Tyr Gly Val Ala Ala Met Gly Gly  
 145 150 155 160  
 Ile Asp Ile Asp Lys Asn Gly Leu Gln Ile Gly Thr Asp Asp Thr Lys  
 165 170 175  
 Asp Gly Asp Asn Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro  
 180 185 190  
 Gln Ile Gly Glu Glu Asn Trp Gln Glu Thr Tyr Ser Tyr Tyr Gly Gly  
 195 200 205  
 Arg Ala Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe  
 210 215 220  
 Ala Arg Pro Thr Asn Val Lys Gly Gly Gln Ala Lys Ile Lys Thr Asp  
 225 230 235 240  
 Gly Asp Val Lys Ser Phe Asp Ile Asp Leu Ala Phe Phe Asp Ile Pro  
 245 250 255  
 Asn Ser Gly Ala Gly Asn Gly Thr Asn Val Asn Asp Asp Pro Asp Met  
 260 265 270  
 Val Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile  
 275 280 285  
 Val Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Glu Val Asn Leu Cys  
 290 295 300  
 Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn  
 305 310 315 320  
 Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu  
 325 330 335  
 Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg  
 340 345 350  
 Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg  
 355 360 365  
 Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro  
 370 375 380  
 Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn  
 385 390 395 400  
 Tyr Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ser Val Tyr Gln Gly  
 405 410 415  
 Val Lys Pro Lys Thr Asp Asn Gly Asn Asp Gln Trp Glu Thr Asp Ser  
 420 425 430  
 Thr Val Ser Ser His Asn Gln Ile Cys Lys Gly Asn Ile Tyr Ala Met  
 435 440 445  
 Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn  
 450 455 460  
 Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile  
 465 470 475 480  
 Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val  
 485 490 495  
 Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp  
 500 505 510  
 Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn  
 515 520 525  
 Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val  
 530 535 540

Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu  
 545 550 555 560  
 Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp  
 565 570 575  
 Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp  
 580 585 590  
 Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe  
 595 600 605  
 Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn  
 610 615 620  
 Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met  
 625 630 635 640  
 Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro  
 645 650 655  
 Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys  
 660 665 670  
 Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val  
 675 680 685  
 Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His  
 690 695 700  
 Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro  
 705 710 715 720  
 Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr  
 725 730 735  
 Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp  
 740 745 750  
 Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly  
 755 760 765  
 Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg  
 770 775 780  
 Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys  
 785 790 795 800  
 Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe  
 805 810 815  
 Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala  
 820 825 830  
 Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr  
 835 840 845  
 Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser  
 850 855 860  
 Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met  
 865 870 875 880  
 Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp  
 885 890 895  
 Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp  
 900 905 910  
 Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr  
 915 920 925  
 Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 930 935 940

&lt;210&gt; 91

&lt;211&gt; 930

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 9 Hexon

&lt;400&gt; 91

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1      5      10      15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
 20      25      30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
 35      40      45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
 50      55      60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
 65      70      75      80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
 85      90      95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
 100     105     110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
 115     120     125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Thr Asp Asn Gln Thr Glu Lys
 130     135     140
Thr Ala Thr Tyr Gly Asn Ala Pro Val Glu Gly Ile Asn Ile Thr Lys
 145     150     155     160
Asp Gly Ile Gln Leu Gly Thr Asp Ser Asp Gly Gln Ala Ile Tyr Ala
 165     170     175
Asp Glu Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Pro Glu Trp His
 180     185     190
---Asp Thr Thr Gly Thr Glu Glu Lys Tyr Gly Gly Arg Ala Leu Lys Pro
 195     200     205
Ala Thr Asp Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn
 210     215     220
- Val Lys Gly Gly Gln Ala Lys Ser Arg Thr Lys Thr Asp Gly Thr Thr
 225     230     235     240
Glu Pro Asp Ile Asp Met Ala Phe Phe Asp Gly Arg Asn Ala Thr Thr
 245     250     255
Ala Gly Leu Thr Pro Glu Ile Val Leu Tyr Thr Glu Asn Val Asp Leu
 260     265     270
Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp Asp Ser
 275     280     285
Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn
 290     295     300
Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser
 305     310     315     320
Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala
 325     330     335
Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu
 340     345     350
Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln
 355     360     365
Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly
 370     375     380
Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asn Ala Val Gly
 385     390     395     400

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Arg	Thr	Asn	Ser	Tyr	Gln	Gly	Ile	Lys	Pro	Asn	Gly	Gly	Asp	Pro	Ala	
				405					410					415		
Thr	Trp	Ala	Lys	Asp	Glu	Ser	Val	Asn	Asp	Ser	Asn	Glu	Leu	Gly	Lys	
			420					425					430			
Gly	Asn	Pro	Phe	Ala	Met	Glu	Ile	Asn	Ile	Gln	Ala	Asn	Leu	Trp	Arg	
			435					440				445				
Asn	Phe	Leu	Tyr	Ala	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	
	450					455					460					
Tyr	Thr	Pro	Ala	Asn	Ile	Thr	Leu	Pro	Ala	Asn	Thr	Asn	Thr	Tyr	Asp	
465					470					475					480	
Tyr	Met	Asn	Gly	Arg	Val	Val	Ala	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Ile	
				485					490					495		
Asn	Ile	Gly	Ala	Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	
			500					505					510			
Phe	Asn	His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	
		515					520					525				
Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	
	530					535				540						
Phe	Ala	Ile	Lys	Ser	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	
545					550					555					560	
Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn	Met	Ile	Leu	Gln	Ser	Ser	Leu	Gly	
				565					570					575		
Asn	Asp	Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	Ala	Phe	Thr	Ser	Ile	Asn	
			580					585					590			
Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	
		595					600					605				
Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	
	610					615				620						
Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	
				630						635					640	
Val	Pro	Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	
				645					650					655		
Ser	Phe	Thr	Arg	Leu	Lys	Thr	Arg	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	
			660					665					670			
Phe	Asp	Pro	Tyr	Phe	Val	Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	
		675					680					685				
Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	Val	Ser	Ile	Thr	Phe	Asp	
		690				695						700				
Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	
705					710					715					720	
Phe	Glu	Ile	Lys	Arg	Thr	Val	Asp	Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	
				725					730					735		
Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe	Leu	Val	Gln	Met	Leu	Ala	His	Tyr	
			740					745					750			
Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr	Val	Pro	Glu	Gly	Tyr	Lys	Asp	Arg	
		755					760					765				
Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe	Gln	Pro	Met	Ser	Arg	Gln	Val	Val	
		770				775						780				
Asp	Glu	Val	Asn	Tyr	Lys	Asp	Tyr	Gln	Ala	Val	Thr	Leu	Ala	Tyr	Gln	
785					790					795					800	
His	Asn	Asn	Ser	Gly	Phe	Val	Gly	Tyr	Leu	Ala	Pro	Thr	Met	Arg	Gln	
				805					810					815		
Gly	Gln	Pro	Tyr	Pro	Ala	Asn	Tyr	Pro	Tyr	Pro	Leu	Ile	Gly	Lys	Ser	
			820					825					830			

Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met  
           835                  840          845  
 Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr  
       850                  855          860  
 Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp  
 865                  870          875          880  
 Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val  
           885                  890          895  
 Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly  
           900                  905          910  
 Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala  
       915                  920          925  
 Thr Thr  
       930

<210> 92

<211> 930

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 10 Hexon

<400> 92

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala  
   1                  5          10          15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
           20                  25          30  
 Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro  
       35                  40          45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
       50                  55          60  
 Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
 65                  70          75          80  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
           85                  90          95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
       100                  105          110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
       115                  120          125  
 Ala Pro Asn Thr Cys Gln Trp Thr Tyr Thr Asp Asn Gln Thr Glu Lys  
       130                  135          140  
 Thr Ala Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser Ile Thr Lys  
 145                  150          155          160  
 Asp Gly Ile Gln Leu Gly Thr Asp Thr Asp Asp Gln Pro Ile Tyr Ala  
           165                  170          175  
 Asp Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala Glu Trp His  
       180                  185          190  
 Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala Leu Lys Pro  
       195                  200          205  
 Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn  
       210                  215          220  
 Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly Gly Thr Lys  
 225                  230          235          240  
 Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser Ala Ala Ala  
           245                  250          255  
 Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn Val Asp Leu  
       260                  265          270

Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp Asp Ser  
 275 280 285  
 Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn  
 290 295 300  
 Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser  
 305 310 315 320  
 Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala  
 325 330 335  
 Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu  
 340 345 350  
 Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln  
 355 360 365  
 Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly  
 370 375 380  
 Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asn Ala Val Gly  
 385 390 395 400  
 Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Ala Asp Gln Thr  
 405 410 415  
 Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu Leu Gly Lys  
 420 425 430  
 Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg  
 435 440 445  
 Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys  
 450 455 460  
 Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Tyr Asp  
 465 470 475 480  
 Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ala Tyr Ile  
 485 490 495  
 Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro  
 500 505 510  
 Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu  
 515 520 525  
 Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe  
 530 535 540  
 Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu  
 545 550 555 560  
 Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly  
 565 570 575  
 Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn  
 580 585 590  
 Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu  
 595 600 605  
 Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr  
 610 615 620  
 Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn  
 625 630 635 640  
 Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp  
 645 650 655  
 Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly  
 660 665 670  
 Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly  
 675 680 685  
 Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp  
 690 695 700

Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu  
 705 710 715 720  
 Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln  
 725 730 735  
 Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr  
 740 745 750  
 Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg  
 755 760 765  
 Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val  
 770 775 780  
 Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln  
 785 790 795 800  
 His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln  
 805 810 815  
 Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser  
 820 825 830  
 Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met  
 835 840 845  
 Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr  
 850 855 860  
 Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp  
 865 870 875 880  
 Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val  
 885 890 895  
 Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly  
 900 905 910  
 Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala  
 915 920 925  
 Thr Thr  
 930

&lt;210&gt; 93

&lt;211&gt; 960

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 11 Hexon

&lt;400&gt; 93

Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr  
 65 70 75 80  
 Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Ser Cys Glu Trp Glu Gln Glu Glu Thr Gln Ala Val Glu  
 130 135 140

Glu Ala Ala Glu Glu Glu Glu Glu Asp Ala Asp Gly Gln Ala Glu Glu  
 145 150 155 160  
 Glu Gln Ala Ala Thr Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu  
 165 170 175  
 Ser Gly Glu Lys Ile Ser Lys Asp Gly Leu Gln Ile Gly Thr Asp Ala  
 180 185 190  
 Thr Ala Thr Glu Gln Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro  
 195 200 205  
 Glu Pro Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val  
 210 215 220  
 Ala Gly Gly Arg Val Leu Lys Lys Thr Thr Pro Met Lys Pro Cys Tyr  
 225 230 235 240  
 Gly Ser Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu  
 245 250 255  
 Ala Ala Asn Ala Gln Gly Gln Leu Glu Ser Gln Val Glu Met Gln Phe  
 260 265 270  
 Phe Ser Thr Ser Glu Asn Ala Arg Asn Glu Ala Asn Asn Ile Gln Pro  
 275 280 285  
 Lys Leu Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr  
 290 295 300  
 His Leu Ser Tyr Lys Pro Thr Lys Ser Asp Asp Asn Ser Lys Val Met  
 305 310 315 320  
 Leu Gly Gln Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg  
 325 330 335  
 Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly  
 340 345 350  
 Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln  
 355 360 365  
 Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly  
 370 375 380  
 Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr  
 385 390 395 400  
 Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu  
 405 410 415  
 Pro Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr  
 420 425 430  
 Gln Ala Val Lys Thr Asn Asn Gly Asn Asn Gly Gly Gln Val Thr Trp  
 435 440 445  
 Thr Lys Asp Glu Thr Phe Ala Glu Arg Asn Glu Ile Gly Val Gly Asn  
 450 455 460  
 Asn Phe Ala Met Glu Ile Asn Leu Asn Ala Asn Leu Trp Arg Asn Phe  
 465 470 475 480  
 Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn  
 485 490 495  
 Pro Ser Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met  
 500 505 510  
 Asn Lys Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu  
 515 520 525  
 Gly Ala Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn  
 530 535 540  
 His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn  
 545 550 555 560  
 Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala  
 565 570 575



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Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn
      580      585      590
Phe Arg Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp
      595      600      605
Leu Arg Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr
      610      615      620
Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala
      625      630      635      640
Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser
      645      650      655
Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro
      660      665      670
Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe
      675      680      685
Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp
      690      695      700
Pro Tyr Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe
      705      710      715      720
Tyr Leu Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser
      725      730      735
Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu
      740      745      750
Ile Lys Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn
      755      760      765
Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile
      770      775      780
Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr
      785      790      795      800
Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln
      805      810      815
Thr Lys Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn
      820      825      830
Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln
      835      840      845
Ala Tyr Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val
      850      855      860
Asp Ser Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg
      865      870      875      880
Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu
      885      890      895
Gly Gln Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr
      900      905      910
Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe
      915      920      925
Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile
      930      935      940
Glu Thr Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
      945      950      955      960

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&lt;210&gt; 94

&lt;211&gt; 944

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 16 Hexon

&lt;400&gt; 94

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1      5      10      15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20      25      30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
35      40      45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50      55      60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65      70      75      80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
85      90      95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
100     105     110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115     120     125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Thr Glu Asn Gly Gly Gly Gln
130     135     140
Ala Thr Thr Lys Thr His Thr Tyr Gly Val Ala Pro Met Gly Gly Thr
145     150     155     160
Asn Ile Thr Val Asp Gly Leu Gln Ile Gly Thr Asp Ala Thr Ala Asp
165     170     175
Thr Glu Lys Pro Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro Gln
180     185     190
Ile Gly Glu Glu Asn Trp Gln Glu Thr Glu Ser Phe Tyr Gly Gly Arg
195     200     205
Ala Leu Lys Lys Asp Thr Asn Met Lys Pro Cys Tyr Gly Ser Phe Ala
210     215     220
Arg Pro Thr Asn Glu Lys Gly Gly Gln Ala Lys Leu Lys Val Gly Ala
225     230     235     240
Asp Gly Leu Pro Thr Lys Glu Phe Asp Ile Asp Leu Ala Phe Phe Asp
245     250     255
Thr Pro Gly Gly Thr Val Thr Gly Gly Thr Glu Glu Tyr Lys Ala Asp
260     265     270
Ile Val Met Tyr Thr Glu Asn Thr Tyr Leu Glu Thr Pro Asp Thr His
275     280     285
Val Val Tyr Lys Pro Gly Lys Asp Asn Thr Ser Ser Lys Ile Asn Leu
290     295     300
Val Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp
305     310     315     320
Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val
325     330     335
Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp
340     345     350
Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp
355     360     365
Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp
370     375     380
Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro
385     390     395     400
Asn Tyr Cys Phe Pro Leu Asp Gly Ser Gly Thr Asn Ala Ala Tyr Gln
405     410     415
Gly Val Lys Val Lys Asn Gly Gln Asp Gly Asp Val Glu Ser Glu Trp
420     425     430

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Glu	Lys	Asp	Asp	Thr	Val	Ala	Ala	Arg	Asn	Gln	Leu	Cys	Lys	Gly	Asn
		435					440					445			
Ile	Phe	Ala	Met	Glu	Ile	Asn	Leu	Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe
	450					455					460				
Leu	Tyr	Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr
465				470						475					480
Pro	Ala	Asn	Ile	Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met
			485						490					495	
Asn	Gly	Arg	Val	Val	Pro	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Ile	Asn	Ile
			500					505					510		
Gly	Ala	Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn
		515					520					525			
His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn
	530					535					540				
Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala
545					550					555					560
Ile	Lys	Ser	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn
			565						570					575	
Phe	Arg	Lys	Asp	Val	Asn	Met	Ile	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp
			580					585					590		
Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn	Leu	Tyr
		595					600					605			
Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala
	610					615						620			
Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser
625					630					635					640
Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro
			645						650					655	
Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ser	Phe
			660					665					670		
Thr	Arg	Leu	Lys	Thr	Lys	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp
		675					680					685			
Pro	Tyr	Phe	Val	Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe
	690					695					700				
Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	Val	Ser	Ile	Thr	Phe	Asp	Ser	Ser
705					710					715					720
Val	Ser	Trp	Pro	Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu
			725						730					735	
Ile	Lys	Arg	Thr	Val	Asp	Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn
			740					745					750		
Met	Thr	Lys	Asp	Trp	Phe	Leu	Val	Gln	Met	Leu	Ala	His	Tyr	Asn	Ile
		755					760					765			
Gly	Tyr	Gln	Gly	Phe	Tyr	Val	Pro	Glu	Gly	Tyr	Lys	Asp	Arg	Met	Tyr
	770					775					780				
Ser	Phe	Phe	Arg	Asn	Phe	Gln	Pro	Met	Ser	Arg	Gln	Val	Val	Asp	Glu
785					790					795					800
Val	Asn	Tyr	Lys	Asp	Tyr	Gln	Ala	Val	Thr	Leu	Ala	Tyr	Gln	His	Asn
			805						810					815	
Asn	Ser	Gly	Phe	Val	Gly	Tyr	Leu	Ala	Pro	Thr	Met	Arg	Gln	Gly	Gln
			820					825					830		
Pro	Tyr	Pro	Ala	Asn	Tyr	Pro	Tyr	Pro	Leu	Ile	Gly	Lys	Ser	Ala	Val
		835					840					845			
Ala	Ser	Val	Thr	Gln	Lys	Lys	Phe	Leu	Cys	Asp	Arg	Val	Met	Trp	Arg
	850					855					860				

Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu  
 865 870 875 880  
 Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn  
 885 890 895  
 Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe  
 900 905 910  
 Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile  
 915 920 925  
 Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 930 935 940

<210> 95

<211> 960

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 17 Hexon

<400> 95

Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr  
 65 70 75 80  
 Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Ser Cys Glu Trp Glu Gln Glu Glu Thr Gln Ala Val Glu  
 130 135 140  
 Glu Ala Ala Glu Glu Glu Glu Glu Asp Ala Asp Gly Gln Ala Glu Glu  
 145 150 155 160  
 Glu Gln Ala Ala Thr Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu  
 165 170 175  
 Ser Gly Glu Lys Ile Ser Lys Asp Gly Leu Gln Ile Gly Thr Asp Ala  
 180 185 190  
 Thr Ala Thr Glu Gln Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro  
 195 200 205  
 Glu Pro Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val  
 210 215 220  
 Ala Gly Gly Arg Val Leu Lys Lys Ser Thr Pro Met Lys Pro Cys Tyr  
 225 230 235 240  
 Gly Ser Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu  
 245 250 255  
 Thr Ala Asn Ala Gln Gly Gln Leu Glu Ser Gln Val Glu Met Gln Phe  
 260 265 270  
 Phe Ser Thr Ser Glu Asn Ala Arg Asn Glu Thr Asn Asn Ile Gln Pro  
 275 280 285  
 Lys Leu Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr  
 290 295 300

His	Leu	Ser	Tyr	Lys	Pro	Ala	Lys	Ser	Asp	Asp	Asn	Ser	Lys	Ile	Met	305	310	315	320
Leu	Gly	Gln	Gln	Ser	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	325	330	335	
Asp	Asn	Phe	Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	340	345	350	
Val	Leu	Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	355	360	365	
Asp	Arg	Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Met	Gly	370	375	380	
Asp	Arg	Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	385	390	395	400
Asp	Pro	Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Thr	Glu	Asp	Glu	Leu	405	410	415	
Pro	Asn	Tyr	Cys	Phe	Pro	Leu	Gly	Gly	Ile	Gly	Val	Thr	Asp	Thr	Tyr	420	425	430	
Gln	Ala	Val	Lys	Thr	Asn	Asn	Gly	Asn	Asn	Gly	Gly	Gln	Val	Thr	Trp	435	440	445	
Thr	Lys	Asp	Glu	Thr	Phe	Ala	Asp	Arg	Asn	Glu	Ile	Gly	Val	Gly	Asn	450	455	460	
Asn	Phe	Ala	Met	Glu	Ile	Asn	Leu	Ser	Ala	Asn	Leu	Trp	Arg	Asn	Phe	465	470	475	480
Leu	Tyr	Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Lys	Leu	Lys	Tyr	Asn	485	490	495	
Pro	Ser	Asn	Val	Asp	Ile	Ser	Asp	Asn	Pro	Asn	Thr	Tyr	Asp	Tyr	Met	500	505	510	
Asn	Lys	Arg	Val	Val	Ala	Pro	Gly	Leu	Val	Asp	Cys	Tyr	Ile	Asn	Leu	515	520	525	
Gly	Ala	Arg	Trp	Ser	Leu	Asp	Tyr	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	530	535	540	
His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	545	550	555	560
Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	565	570	575	
Ile	Lys	Asn	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn		580	585	590	
Phe	Arg	Lys	Asp	Val	Asn	Met	Val	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	595	600	605	
Leu	Arg	Val	Asp	Gly	Ala	Ser	Ile	Lys	Phe	Glu	Ser	Ile	Cys	Leu	Tyr	610	615	620	
Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	625	630	635	640
Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	645	650	655	
Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	660	665	670	
Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ala	Phe	675	680	685	
Thr	Arg	Leu	Lys	Thr	Lys	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	690	695	700	
Pro	Tyr	Tyr	Thr	Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	705	710	715	720
Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	Val	Ser	Val	Thr	Phe	Asp	Ser	Ser	725	730	735	

Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu  
 740 745 750  
 Ile Lys Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn  
 755 760 765  
 Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile  
 770 775 780  
 Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr  
 785 790 795 800  
 Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln  
 805 810 815  
 Thr Lys Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn  
 820 825 830  
 Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln  
 835 840 845  
 Ala Tyr Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val  
 850 855 860  
 Asp Ser Ile Thr Gln Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg  
 865 870 875 880  
 Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Ser Asp Leu  
 885 890 895  
 Gly Gln Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr  
 900 905 910  
 Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe  
 915 920 925  
 Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile  
 930 935 940  
 Glu Thr Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 945 950 955 960

&lt;210&gt; 96

&lt;211&gt; 958

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 19 Hexon

&lt;400&gt; 96

Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr  
 65 70 75 80  
 Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Ser Cys Glu Trp Glu Gln Leu Glu Glu Ala Gln Ala Ala  
 130 135 140  
 Leu Glu Asp Glu Glu Leu Glu Asp Glu Asp Glu Glu Pro Gln Asp Glu  
 145 150 155 160

Ala Pro Val Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu Ser Gly  
 165 170 175  
 Glu Glu Ile Thr Lys Asp Gly Leu Gln Ile Gly Ser Asp Asn Thr Glu  
 180 185 190  
 Ala Gln Ser Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro Glu Pro  
 195 200 205  
 Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val Ala Gly  
 210 215 220  
 Gly Arg Val Leu Lys Lys Thr Thr Pro Met Lys Pro Cys Tyr Gly Ser  
 225 230 235 240  
 Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu Val Ala  
 245 250 255  
 Asp Asp Lys Gly Val Leu Gln Ser Lys Val Glu Leu Gln Phe Phe Ser  
 260 265 270  
 Asn Thr Thr Thr Leu Asn Gln Arg Glu Gly Asn Asp Thr Lys Pro Lys  
 275 280 285  
 Val Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr His  
 290 295 300  
 Ile Ser Tyr Lys Pro Thr Lys Ser Asp Asp Asn Ser Lys Val Met Leu  
 305 310 315 320  
 Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp  
 325 330 335  
 Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val  
 340 345 350  
 Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp  
 355 360 365  
 Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly Asp  
 370 375 380  
 Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp  
 385 390 395 400  
 Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu Pro  
 405 410 415  
 Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr Gln  
 420 425 430  
 Val Ile Lys Thr Asn Gly Asn Gly Gln Ala Asp Pro Thr Trp Glu Lys  
 435 440 445  
 Asp Thr Glu Phe Ala Asp Arg Asn Glu Ile Gly Val Gly Asn Asn Phe  
 450 455 460  
 Ala Met Glu Ile Asn Leu Asn Ala Asn Leu Trp Arg Asn Phe Leu Tyr  
 465 470 475 480  
 Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn Pro Ser  
 485 490 495  
 Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met Asn Lys  
 500 505 510  
 Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu Gly Ala  
 515 520 525  
 Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn His His  
 530 535 540  
 Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg  
 545 550 555 560  
 Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys  
 565 570 575  
 Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg  
 580 585 590

Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg  
 595 600 605  
 Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr Ala Thr  
 610 615 620  
 Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu  
 625 630 635 640  
 Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala  
 645 650 655  
 Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser  
 660 665 670  
 Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe Thr Arg  
 675 680 685  
 Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr  
 690 695 700  
 Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu  
 705 710 715 720  
 Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser Val Ser  
 725 730 735  
 Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys  
 740 745 750  
 Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr  
 755 760 765  
 Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr  
 770 775 780  
 Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr Ser Phe  
 785 790 795 800  
 Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln Thr Lys  
 805 810 815  
 Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn Asn Ser  
 820 825 830  
 Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln Ala Tyr  
 835 840 845  
 Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val Asp Ser  
 850 855 860  
 Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg Ile Pro  
 865 870 875 880  
 Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln  
 885 890 895  
 Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu  
 900 905 910  
 Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val  
 915 920 925  
 Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Thr  
 930 935 940  
 Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 945 950 955

&lt;210&gt; 97

&lt;211&gt; 2865

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 8 Hexon

&lt;400&gt; 97

atggccaccc catcgatgtt gcccagtg gcatacatgc acatcgccgg acaggatgct 60  
 tcggagtacc tgagtccggg tctggtgcag ttcgccgtg ccacagacac ctacttcaat 120



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ctggggaaca agtttaggaa cccaccgtg gccccaccc acgatgtgac caccgaccga 180
agccagcggc tgatgctgcg ctttgtgccc gttgatcggg aggacaatac ctactcatac 240
aaagttcgct acacactggc tgtgggcgac aacagagtgc tggatatggc cagcaccttc 300
tttgacatcc ggggggtgct tgacagaggt cccagtttca agccatactc tggcacggct 360
tacaactcct tggctcctaa gggtgccccc aatacatgcc agtggatagc taaagggctg 420
cccgttcaag atgatgctga acaagctcag gaacaaaaag atgttaccta tacttttggc 480
aatgcgccag taaaagcaga agatgacatt acaaaagacg gattagaagt aggcatacaa 540
attattgggtg atgaggagaa tcccatttat gcagataaaa catatcaacc agagccacag 600
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caatgggaaa aaaataccga agtaaattgga gctaattgaa taggaaaggg aaacaattat 1380
gcaatggaaa ttaatctaca agctaaccctc tggagaagtt ttctttactc caacgtggct 1440
ctgtatcttc cagacggtta caaatatacc ccagccaatg ttacgtctgc agacaacaaa 1500
aatacctatg ggtacataaa cggacgagta gtgtctccat ctttgggtgga ttcatacatc 1560
aacattggag ccagatggtc tttggactct atggacaatg tcaaccatt taatcaccac 1620
cgcaatgctg ggctgcgcta ccgttccatt cttcttggca atggacgcta tgtgcccttc 1680
cacatccaag tgccgcagaa attctttgct atcaagaact tgctgcttct gccaggctcc 1740
tacacctatg agtggaaact cagaaaggat gtgaacatgg tcctacaaag ttcccttgg 1800
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aatgccacta acattcccat ctccattccc tctcgcaact gggctgcctt caggggctgg 2040
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tttgtctatt caggctccat tccctacct gatggtacct tctacctcaa ccacactttc 2160
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catgcgctgg acatgacttt tgaggtggat cccatggatg agccacact gctttatctt 2760
ctttttgaag tcttcgacgt ggtcagagtg caccagccac accgcggcgt catcgaggct 2820
gtctacctgc gtacccatt ctcagctggt aacgccacca cataa 2865

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&lt;210&gt; 98

&lt;211&gt; 954

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus ChAd 8

&lt;400&gt; 98

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1           5           10           15

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Gly	Gln	Asp	Ala	Ser	Glu	Tyr	Leu	Ser	Pro	Gly	Leu	Val	Gln	Phe	Ala	
			20					25					30			
Arg	Ala	Thr	Asp	Thr	Tyr	Phe	Asn	Leu	Gly	Asn	Lys	Phe	Arg	Asn	Pro	
		35					40					45				
Thr	Val	Ala	Pro	Thr	His	Asp	Val	Thr	Thr	Asp	Arg	Ser	Gln	Arg	Leu	
		50				55					60					
Met	Leu	Arg	Phe	Val	Pro	Val	Asp	Arg	Glu	Asp	Asn	Thr	Tyr	Ser	Tyr	
65					70					75					80	
Lys	Val	Arg	Tyr	Thr	Leu	Ala	Val	Gly	Asp	Asn	Arg	Val	Leu	Asp	Met	
				85					90					95		
Ala	Ser	Thr	Phe	Phe	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Pro	Ser	
			100					105					110			
Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly	
		115					120					125				
Ala	Pro	Asn	Thr	Cys	Gln	Trp	Ile	Ala	Lys	Gly	Ser	Pro	Val	Gln	Asp	
		130				135					140					
Asp	Ala	Glu	Gln	Ala	Gln	Glu	Gln	Lys	Asp	Val	Thr	Tyr	Thr	Phe	Gly	
145					150					155					160	
Asn	Ala	Pro	Val	Lys	Ala	Glu	Asp	Asp	Ile	Thr	Lys	Asp	Gly	Leu	Glu	
				165					170					175		
Val	Gly	Ile	Gln	Ile	Ile	Gly	Asp	Glu	Glu	Asn	Pro	Ile	Tyr	Ala	Asp	
			180					185					190			
Lys	Thr	Tyr	Gln	Pro	Glu	Pro	Gln	Val	Gly	Asp	Glu	Gln	Trp	His	Asp	
		195					200					205				
Thr	Thr	Gly	Thr	Thr	Glu	Gln	Tyr	Gly	Gly	Arg	Ala	Leu	Lys	Pro	Ala	
		210				215					220					
Thr	Asn	Met	Arg	Pro	Cys	Tyr	Gly	Ser	Phe	Ala	Arg	Pro	Thr	Asn	Lys	
225					230					235					240	
Lys	Gly	Gly	Gln	Ala	Lys	Thr	Arg	Lys	Val	Glu	Lys	Thr	Glu	Gly	Asp	
				245					250					255		
Lys	Lys	Thr	Glu	Val	Glu	Glu	Leu	Asp	Ile	Asp	Met	Asp	Phe	Tyr	Asp	
			260					265					270			
Ala	Arg	Ser	Lys	Lys	Gln	Gly	Tyr	Asp	Pro	Gln	Ile	Val	Leu	Tyr	Ser	
		275					280					285				
Glu	Asn	Val	Asn	Leu	Glu	Thr	Pro	Asp	Thr	His	Ile	Val	Tyr	Lys	Pro	
		290				295					300					
Gly	Thr	Asp	Glu	Thr	Ser	Ser	Ser	Thr	Asn	Leu	Gly	Gln	Gln	Ala	Met	
305					310					315					320	
Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe	Ile	Gly	Leu	
				325					330					335		
Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala	Gly	Gln	Ala	
			340					345					350			
Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn	Thr	Glu	Leu	
		355					360					365				
Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly	Asp	Arg	Thr	Arg	Tyr	Phe	
		370				375					380					
Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	Val	Arg	Ile	
385					390					395					400	
Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu	Pro	Asn	Tyr	Cys	Phe	Pro	
			405						410					415		
Leu	Asp	Gly	Val	Gly	Pro	Ile	Thr	Glu	Thr	Tyr	Gln	Gly	Ile	Lys	Pro	
			420					425					430			
Lys	Thr	Ala	Asp	Asn	Ala	Asn	Asp	Gln	Trp	Glu	Lys	Asn	Thr	Glu	Val	
		435					440					445				

Asn	Gly	Ala	Asn	Glu	Ile	Gly	Lys	Gly	Asn	Asn	Tyr	Ala	Met	Glu	Ile		
450						455					460						
Asn	Leu	Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr	Ser	Asn	Val	Ala		
465					470					475					480		
Leu	Tyr	Leu	Pro	Asp	Gly	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	Val	Thr	Leu		
				485					490					495			
Pro	Asp	Asn	Lys	Asn	Thr	Tyr	Gly	Tyr	Ile	Asn	Gly	Arg	Val	Val	Ser		
			500					505					510				
Pro	Ser	Leu	Val	Asp	Ser	Tyr	Ile	Asn	Ile	Gly	Ala	Arg	Trp	Ser	Leu		
		515					520					525					
Asp	Leu	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn	Ala	Gly		
	530					535					540						
Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe		
545					550					555					560		
His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys	Asn	Leu	Leu	Leu		
				565					570					575			
Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn		
			580					585					590				
Met	Val	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Thr	Asp	Gly	Ala		
		595					600					605					
Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met		
	610					615					620						
Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr		
625					630					635					640		
Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr		
				645					650					655			
Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Ile	Pro	Ile	Ser	Ile	Pro	Ser	Arg		
			660					665					670				
Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	Lys	Thr	Lys		
		675					680					685					
Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Phe	Val	Tyr	Ser		
	690				695						700						
Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe		
705					710					715					720		
Lys	Lys	Val	Ser	Ile	Met	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn		
				725					730					735			
Asp	Arg	Leu	Leu	Cys	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	Thr	Val	Asp		
		740						745					750				
Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe		
	755					760						765					
Leu	Val	Gln	Met	Leu	Ala	Asn	Tyr	Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr		
	770					775					780						
Ile	Pro	Glu	Gly	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe		
785					790					795					800		
Gln	Pro	Met	Ser	Arg	Gln	Val	Val	Asp	Glu	Val	Asn	Tyr	Lys	Glu	Tyr		
				805					810					815			
Gln	Ala	Val	Thr	Leu	Ala	Tyr	Gln	His	Asn	Asn	Ser	Gly	Phe	Val	Gly		
			820					825					830				
Tyr	His	Ala	Pro	Thr	Leu	Arg	Gln	Gly	Gln	Pro	Tyr	Pro	Ala	Asn	Tyr		
	835						840					845					
Pro	Tyr	Pro	Leu	Ile	Gly	Thr	Thr	Ala	Val	Thr	Ser	Val	Thr	Gln	Lys		
	850					855					860						
Lys	Phe	Leu	Cys	Asp	Arg	Thr	Met	Trp	Arg	Ile	Pro	Phe	Ser	Ser	Asn		
865					870					875					880		

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<210> 99
<211> 2871
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 22 Hexon
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ctggggaaca	agtttaggaa	ccctaccgtg	gcgcccaccc	atgatgtgac	caccgaccgc	180
agtcaacggc	tgatgctccg	ctttgtgccc	gttgaccggg	aggacaatac	ctactcatac	240
aaagtctcat	acaccttggc	tgtggggcgac	aacagagtgc	tggatatggc	cagtactttt	300
tttgacattc	ggggtgtgtt	ggatagaggc	ccatagcttca	agccatattc	tggcactgtc	360
tacaactcat	tggcccctaa	gggcgctccc	aatacattctc	agtggaattgc	tgaaggcgta	420
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ctcgggtcaac	aatctatgcc	caacagaccc	aactacattg	gcttttagaga	taacttttatt	1020
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ttgaatgcgg	tggttgactt	gcaggacaga	aacacagaac	tatcatatca	actactgctt	1140
gattctcttg	gtgacagaac	cagatacttc	agcatgtgga	atcaagcagt	cgatagctat	1200
gatcctgatg	tgcgattat	tgaaaattct	ggggtggaag	atgagcttcc	caactactgc	1260
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gagggtgcag	attggaagaa	gcctgacata	aatggaacaa	gtgaaattgg	acaaggaaat	1380
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ccctattttg	tttactcttg	ttctataact	tacctggatg	gtaccttcta	ccttaaccac	2160
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ttgctaactc	caaatgagtt	cgaatcaag	cgcacaattg	atggggaagg	ctacaattgt	2280

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&lt;210&gt; 100

&lt;211&gt; 956

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 22 Hexon

&lt;400&gt; 100

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Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
          20          25          30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
          35          40          45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
          50          55          60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65          70          75          80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
          85          90          95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
          100         105         110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
          115         120         125
Ala Pro Asn Thr Ser Gln Trp Ile Ala Glu Gly Val Lys Lys Glu Asn
          130         135         140
Gly Glu Ala Asp Asn Glu Ala Ala Val Glu Glu Glu Glu Glu Lys
145          150         155         160
Asn Leu Thr Thr Tyr Thr Phe Gly Asn Ala Pro Val Lys Ala Glu Gly
          165         170         175
Gly Asp Ile Thr Lys Asp Lys Gly Leu Pro Ile Gly Ser Glu Ile Thr
          180         185         190
Asp Gly Glu Ala Lys Pro Ile Tyr Ala Asp Lys Leu Tyr Gln Pro Glu
          195         200         205
Pro Gln Val Gly Glu Glu Thr Trp Thr Asp Thr Asp Gly Thr Thr Glu
          210         215         220
Lys Tyr Gly Gly Arg Ala Leu Lys Pro Glu Thr Lys Met Lys Pro Cys
225          230         235         240
Tyr Gly Ser Phe Ala Lys Pro Thr Asn Val Lys Gly Gly Gln Ala Lys
          245         250         255
Gln Lys Thr Thr Glu Gln Leu Gln Asn Gln Gln Val Glu Tyr Asp Ile
          260         265         270
Asp Met Asn Phe Phe Asp Gln Ala Ser Gln Lys Ala Asn Phe Ser Pro
          275         280         285
Lys Ile Val Met Tyr Ala Glu Asn Val Asp Leu Glu Thr Pro Asp Thr
          290         295         300

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His	Val	Val	Tyr	Lys	Pro	Gly	Thr	Ser	Glu	Glu	Ser	Ser	His	Ala	Asn
305					310					315					320
Leu	Gly	Gln	Gln	Ser	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg
				325					330					335	
Asp	Asn	Phe	Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly
			340					345					350		
Val	Leu	Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln
		355					360					365			
Asp	Arg	Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly
	370					375						380			
Asp	Arg	Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr
385					390					395					400
Asp	Pro	Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu
				405				410						415	
Pro	Asn	Tyr	Cys	Phe	Pro	Leu	Asp	Gly	Val	Gly	Val	Pro	Thr	Thr	Ser
			420					425					430		
Tyr	Lys	Ile	Ile	Glu	Pro	Asn	Gly	Glu	Gly	Ala	Asp	Trp	Lys	Glu	Pro
	435						440					445			
Asp	Ile	Asn	Gly	Thr	Ser	Glu	Ile	Gly	Gln	Gly	Asn	Leu	Phe	Ala	Met
	450					455					460				
Glu	Ile	Asn	Leu	Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr	Ser	Asn
465					470					475					480
Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	Val
				485					490					495	
Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Gly	Arg	Val
			500					505					510		
Val	Pro	Pro	Ser	Leu	Val	Asp	Thr	Tyr	Val	Asn	Ile	Gly	Ala	Arg	Trp
		515					520					525			
Ser	Leu	Asp	Ala	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn
	530					535					540				
Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val
545					550					555					560
Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Val	Lys	Asn	Leu
				565					570					575	
Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp
			580					585					590		
Val	Asn	Met	Val	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Val	Asp
		595					600					605			
Gly	Ala	Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	Phe
	610					615					620				
Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn
625					630					635					640
Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met
				645					650					655	
Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	Pro
			660					665					670		
Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	Lys
		675					680					685			
Thr	Lys	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Phe	Val
	690					695					700				
Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His
705					710					715					720
Thr	Phe	Lys	Lys	Val	Ser	Ile	Met	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro
				725					730					735	

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<210> 101
<211> 2865
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 24 Hexon
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- 147 -

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cagtgggaaa aagattcaga atttttcagat aaaaa tgaaa taagagtggg aaacaacttc 1380
gctatggaaa tcaacatcaa tgccaacctg tggag gaact tcctgtactc caacgtggcc 1440
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ctgttcgaag tctttgacgt ggtccgggtc caccagccgc accgcggcgt catcgagacc 2820
gtgtacctgc gcacgccctt ctccggcggc aacgc cacca cctaa 2865

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&lt;210&gt; 102

&lt;211&gt; 954

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 24 Hexon

&lt;400&gt; 102

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Gly Gln Asp  Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
  20              25              30
Arg Ala Thr  Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
  35              40              45
Thr Val Ala  Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
  50              55              60
Thr Leu Arg  Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
  65              70              75              80
Lys Ala Arg  Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
  85              90              95
Ala Ser Thr  Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
  100             105             110
Phe Lys Pro  Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
  115             120             125
Ala Pro Asn  Pro Cys Glu Trp Asp Glu Ala Ala Thr Ala Leu Asp Ile
  130             135             140
Asp Leu Asn  Ala Glu Glu Asp Glu Glu Gly Asp Glu Ala Gln Gly Glu
  145             150             155             160

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Gln	Asn	Ile	Thr	Lys	Glu	Gly	Ile	Gln	Ile	Gly	Ile	Asp	Ala	Thr	Ser	
			180					185					190			
Gln	Ala	Gln	Thr	Pro	Leu	Tyr	Ala	Asp	Lys	Thr	Phe	Gln	Pro	Glu	Pro	
		195					200					205				
Gln	Val	Gly	Glu	Ser	Gln	Trp	Asn	Glu	Thr	Glu	Ile	Ser	His	Gly	Ala	
	210					215					220					
Gly	Arg	Val	Leu	Lys	Lys	Thr	Thr	Leu	Met	Lys	Pro	Cys	Tyr	Gly	Ser	
225				230						235					240	
Tyr	Ala	Arg	Pro	Thr	Asn	Glu	Asn	Gly	Gly	Gln	Gly	Ile	Leu	Leu	Glu	
				245					250					255		
Gln	Asp	Gly	Lys	Lys	Glu	Ser	Gln	Val	Glu	Met	Gln	Phe	Phe	Ser	Thr	
			260					265					270			
Thr	Gln	Ala	Ala	Gly	Asn	Ser	Asp	Asn	Pro	Thr	Pro	Lys	Leu	Val		
	275					280					285					
Leu	Tyr	Ser	Glu	Asp	Val	Asn	Leu	Glu	Thr	Pro	Asp	Thr	His	Ile	Ser	
	290					295					300					
Tyr	Met	Pro	Thr	Asn	Asn	Glu	Thr	Asn	Ser	Arg	Glu	Leu	Leu	Gly	Gln	
305				310					315						320	
Gln	Ala	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe	
				325					330					335		
Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala	
		340						345				350				
Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn	
	355					360					365					
Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Met	Gly	Asp	Arg	Thr	
	370					375					380					
Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	
385				390						395				400		
Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Thr	Glu	Asp	Glu	Leu	Pro	Asn	Tyr	
				405					410					415		
Cys	Phe	Pro	Leu	Gly	Gly	Ile	Ile	Asn	Thr	Glu	Thr	Phe	Thr	Lys	Val	
		420						425					430			
Lys	Pro	Lys	Ala	Gly	Gln	Asp	Ala	Gln	Trp	Glu	Lys	Asp	Ser	Glu	Phe	
	435						440					445				
Ser	Asp	Lys	Asn	Glu	Ile	Arg	Val	Gly	Asn	Asn	Phe	Ala	Met	Glu	Ile	
	450					455					460					
Asn	Ile	Asn	Ala	Asn	Leu	Trp	Arg	Asn	Phe	Leu	Tyr	Ser	Asn	Val	Ala	
465				470					475					480		
Leu	Tyr	Leu	Pro	Asp	Lys	Leu	Lys	Tyr	Thr	Pro	Ser	Asn	Val	Gln	Ile	
				485					490					495		
Ser	Asn	Asn	Pro	Asn	Ser	Tyr	Asp	Tyr	Met	Asn	Lys	Arg	Val	Val	Ala	
		500						505					510			
Pro	Gly	Leu	Val	Asp	Cys	Tyr	Ile	Asn	Leu	Gly	Ala	Arg	Trp	Ser	Leu	
	515						520					525				
Asp	Tyr	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn	Ala	Gly	
	530					535					540					
Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe	
545				550					555					560		
His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys	Asn	Leu	Leu	Leu	
				565					570					575		
Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn	
		580						585					590			

Met	Val	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Val	Asp	Gly	Ala		
		595					600					605					
Ser	Ile	Lys	Phe	Glu	Ser	Ile	Cys	Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met		
	610					615					620						
Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr		
625					630					635					640		
Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr		
				645						650					655		
Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	Pro	Ser	Arg		
			660					665					670				
Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ala	Phe	Thr	Arg	Leu	Lys	Thr	Lys		
		675					680					685					
Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Tyr	Thr	Tyr	Ser		
	690					695					700						
Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe		
705					710					715					720		
Lys	Lys	Val	Ser	Val	Thr	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn		
				725						730				735			
Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	Ser	Val	Asp		
			740					745					750				
Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe		
		755					760					765					
Leu	Val	Gln	Met	Leu	Ala	Asn	Tyr	Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr		
	770					775					780						
Ile	Pro	Glu	Ser	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe		
785					790					795					800		
Gln	Pro	Met	Ser	Arg	Gln	Val	Val	Asp	Gln	Thr	Lys	Tyr	Lys	Asp	Tyr		
				805					810					815			
Gln	Glu	Val	Gly	Ile	Ile	His	Gln	His	Asn	Asn	Ser	Gly	Phe	Val	Gly		
			820					825					830				
Tyr	Leu	Ala	Pro	Thr	Met	Arg	Glu	Gly	Gln	Ala	Tyr	Pro	Ala	Asn	Phe		
		835					840					845					
Pro	Tyr	Pro	Leu	Ile	Gly	Lys	Thr	Ala	Val	Asp	Ser	Ile	Thr	Gln	Lys		
	850					855					860						
Lys	Phe	Leu	Cys	Asp	Arg	Thr	Leu	Trp	Arg	Ile	Pro	Phe	Ser	Ser	Asn		
865					870					875					880		
Phe	Met	Ser	Met	Gly	Ala	Leu	Thr	Asp	Leu	Gly	Gln	Asn	Leu	Leu	Tyr		
				885					890						895		
Ala	Asn	Ser	Ala	His	Ala	Leu	Asp	Met	Thr	Phe	Glu	Val	Asp	Pro	Met		
			900					905					910				
Asp	Glu	Pro	Thr	Leu	Leu	Tyr	Val	Leu	Phe	Glu	Val	Phe	Asp	Val	Val		
		915					920					925					
Arg	Val	His	Gln	Pro	His	Arg	Gly	Val	Ile	Glu	Thr	Val	Tyr	Leu	Arg		
	930					935					940						
Thr	Pro	Phe	Ser	Ala	Gly	Asn	Ala	Thr	Thr								
945					950												

&lt;210&gt; 103

&lt;211&gt; 2841

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 26 Hexon

&lt;400&gt; 103

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ctggggaaca agtttaggaa ccccaagggtg gcgcccacgc acgatgtgac caccgaccgc 180
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aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc tggacatggc cagcacctac 300
tttgacatcc gcggcgtgct ggaccggggc cctagcttca aaccctactc cggcaccgcc 360
tacaacagcc tgggtcccaa gggagcacc ccaattccagcc agtgggagca aaaaaagaca 420
ggcaataaca atggaaatgg cggcactgaa tctgttacct ttggtgtagc cgccatgggc 480
ggagagaata ttacaaaaga gggctcttcaa attggaagtg atgaaactaa aaccgataac 540
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caagacggtg tgcagactac agaatatgac atcgacctgg ctttctttga tattccaagc 780
accggcacag ggggcaatgg tacaaatgta aatgataagc cagacatggg catgtacact 840
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tcaagtatta accagatatg caaggggaac atctatgcca tggaaatcaa cattcaagc 1380
aacctgtgga gaagtctcct ttactcgaac gtggccctgt acctgcccga ctcttacaag 1440
tacacgccgg ccaacatcac cctgcccacc aacaccaaca cctacgatta catgaacgg 1500
cgggtggtgc ctccctcgct ggtggacgcc tacatcaaca tcggggcgcg ctggctcgctg 1560
gaccccatgg acaacgtcaa tcccttcaac caccaccgca acgcgggcct gcgctaccgc 1620
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ttcgccatca agagcctcct gctcctgccc gggctcctaca cctacgagtg gaacttcgc 1740
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gcttccacgc tcgaggccat gctgcgcaac gacaccaacg accagtcctt caacgactac 1920
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atccctcgcg gcaactgggc cgccttcgcg ggctggctct tcacgcgtct caagaccaag 2040
gaaacgccct cgctgggctc cgggttcgac ccctacttcg tctactcggg ctccatcccc 2100
tacctcgacg gcaccttcta cctcaaccac accttcaaga aggtctccat caccttcgac 2160
tcctccgtca gctggcccgg caacgaccgg ctctgacgc ccaacgagtt cgaaatcaag 2220
cgcacgctcg acggcgaggg ctacaacgtg gccagtgca acatgacca ggactgggtc 2280
ctggtccaga tgctggccca ctacaacatc ggctaccagg gcttctacgt gcccgagggc 2340
tacaaggacc gcatgtactc cttcttcgcg aacttccagc ccatgagccg ccagggtgg 2400
gacgaggtca actacaagga ctaccaggcc gtcaccttgg cctacCagca caacaactcg 2460
ggcttcgtcg gctacctcgc gccaccatg cgccagggcc agccctaccc cgccaactac 2520
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gacctgggcc agaacatgct ctatgccaac tccgccacg cgctagacat gaatttcgaa 2700
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&lt;210&gt; 104

&lt;211&gt; 946

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 26 Hexon

&lt;400&gt; 104

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala

1

5

10

15

Gly	Gln	Asp	Ala	Ser	Glu	Tyr	Leu	Ser	Pro	Gly	Leu	Val	Gln	Phe	Ala		
			20					25					30				
Arg	Ala	Thr	Asp	Thr	Tyr	Phe	Ser	Leu	Gly	Asn	Lys	Phe	Arg	Asn	Pro		
		35					40					45					
Thr	Val	Ala	Pro	Thr	His	Asp	Val	Thr	Thr	Asp	Arg	Ser	Gln	Arg	Leu		
		50				55					60						
Thr	Leu	Arg	Phe	Val	Pro	Val	Asp	Arg	Glu	Asp	Asn	Thr	Tyr	Ser	Tyr		
65						70				75					80		
Lys	Val	Arg	Tyr	Thr	Leu	Ala	Val	Gly	Asp	Asn	Arg	Val	Leu	Asp	Met		
				85					90					95			
Ala	Ser	Thr	Tyr	Phe	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Pro	Ser		
			100					105					110				
Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly		
		115					120					125					
Ala	Pro	Asn	Ser	Ser	Gln	Trp	Glu	Gln	Lys	Lys	Thr	Gly	Asn	Asn	Asn		
		130				135					140						
Gly	Asn	Gly	Gly	Thr	Glu	Ser	Val	Thr	Phe	Gly	Val	Ala	Ala	Met	Gly		
145					150					155					160		
Gly	Glu	Asn	Ile	Thr	Lys	Glu	Gly	Leu	Gln	Ile	Gly	Ser	Asp	Glu	Thr		
				165					170					175			
Lys	Thr	Asp	Asn	Lys	Glu	Ile	Tyr	Ala	Asp	Lys	Thr	Tyr	Gln	Pro	Glu		
			180					185					190				
Pro	Gln	Ile	Gly	Glu	Glu	Asn	Trp	Gln	Glu	Thr	Phe	Ser	Phe	Tyr	Gly		
		195				200					205						
Gly	Arg	Ala	Leu	Lys	Lys	Asp	Thr	Lys	Met	Lys	Pro	Cys	Tyr	Gly	Ser		
		210				215					220						
Phe	Ala	Arg	Pro	Thr	Asn	Glu	Lys	Gly	Gly	Gln	Ala	Lys	Phe	Lys	Val		
225					230					235					240		
Gln	Asp	Gly	Val	Gln	Thr	Thr	Glu	Tyr	Asp	Ile	Asp	Leu	Ala	Phe	Phe		
				245					250					255			
Asp	Ile	Pro	Ser	Thr	Gly	Thr	Gly	Gly	Asn	Gly	Thr	Asn	Val	Asn	Asp		
			260					265					270				
Lys	Pro	Asp	Met	Val	Met	Tyr	Thr	Glu	Asn	Val	Asn	Leu	Glu	Thr	Pro		
		275					280					285					
Asp	Thr	His	Ile	Val	Tyr	Lys	Pro	Gly	Thr	Ser	Asp	Asp	Ser	Ser	Lys		
		290				295					300						
Ala	Asn	Leu	Cys	Gln	Gln	Ala	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly		
305					310					315					320		
Phe	Arg	Asp	Asn	Phe	Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn		
				325					330					335			
Met	Gly	Val	Leu	Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp		
			340					345					350				
Leu	Gln	Asp	Arg	Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser		
		355					360					365					
Leu	Gly	Asp	Arg	Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp		
		370				375					380						
Ser	Tyr	Asp	Pro	Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Val	Glu	Asp		
385					390					395					400		
Glu	Leu	Pro	Asn	Tyr	Cys	Phe	Pro	Leu	Asp	Gly	Ala	Gly	Thr	Asn	Ala		
				405					410					415			
Val	Tyr	Gln	Gly	Val	Lys	Ala	Lys	Asp	Asn	Gly	Asn	Ala	Ala	Asn	Gly		
			420					425					430				
Asn	Trp	Glu	Gln	Asp	Thr	Gly	Val	Ser	Ser	Ile	Asn	Gln	Ile	Cys	Lys		
		435					440					445					

Gly	Asn	Ile	Tyr	Ala	Met	Glu	Ile	Asn	Ile	Gln	Ala	Asn	Leu	Trp	Arg
450						455				460					
Ser	Phe	Leu	Tyr	Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys
465					470					475					480
Tyr	Thr	Pro	Ala	Asn	Ile	Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp
				485					490					495	
Tyr	Met	Asn	Gly	Arg	Val	Val	Pro	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Ile
			500					505					510		
Asn	Ile	Gly	Ala	Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro
		515					520					525			
Phe	Asn	His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu
	530				535						540				
Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe
545					550					555					560
Phe	Ala	Ile	Lys	Ser	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu
				565					570					575	
Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn	Met	Ile	Leu	Gln	Ser	Ser	Leu	Gly
			580					585					590		
Asn	Asp	Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn
		595				600					605				
Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu
	610					615					620				
Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr
625					630					635					640
Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn
				645					650					655	
Val	Pro	Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp
			660					665					670		
Ser	Phe	Thr	Arg	Leu	Lys	Thr	Lys	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly
		675				680						685			
Phe	Asp	Pro	Tyr	Phe	Val	Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly
	690					695					700				
Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	Val	Ser	Ile	Thr	Phe	Asp
705					710					715					720
Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu
				725					730					735	
Phe	Glu	Ile	Lys	Arg	Thr	Val	Asp	Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln
			740					745					750		
Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe	Leu	Val	Gln	Met	Leu	Ala	His	Tyr
	755					760						765			
Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr	Val	Pro	Glu	Gly	Tyr	Lys	Asp	Arg
	770				775						780				
Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe	Gln	Pro	Met	Ser	Arg	Gln	Val	Val
785					790					795					800
Asp	Glu	Val	Asn	Tyr	Lys	Asp	Tyr	Gln	Ala	Val	Thr	Leu	Ala	Tyr	Gln
			805						810					815	
His	Asn	Asn	Ser	Gly	Phe	Val	Gly	Tyr	Leu	Ala	Pro	Thr	Met	Arg	Gln
			820					825					830		
Gly	Gln	Pro	Tyr	Pro	Ala	Asn	Tyr	Pro	Tyr	Pro	Leu	Ile	Gly	Lys	Ser
		835				840						845			
Ala	Val	Thr	Ser	Val	Thr	Gln	Lys	Lys	Phe	Leu	Cys	Asp	Arg	Val	Met
	850					855					860				
Trp	Arg	Ile	Pro	Phe	Ser	Ser	Asn	Phe	Met	Ser	Met	Gly	Ala	Leu	Thr
865					870					875					880

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<210> 105
<211> 2838
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 30 Hexon
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- 154 -

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aaggatcgca tgtattcctt cttcagaaac ttccagccca tgagcagaca ggtgggtgat 24 00
gaagttaatt acaaggagta ccaagccgtc acacttgctt accaacacaa caactctggc 24 60
tttgtgggtt accttgacc cactatgagg cagggagAAC cttaccccg c taactaccca 25 20
taccocctaa tcggaaccac tgctgttaag agtggtacccc acaaaaagtt cctgtgcgac 25 80
aggaccatgt ggcgcacccc cttctccagc aacttcatgt ccatgggtgc ccttaccgac 26 40
ctgggacaga acatgcttta tgccaactca tcccatgcgc tggacatgac ttttgagggtg 27 00
gatcccatgg atgagcccac cctgctttat cttcttttcg aagttttcga cgtggtcaga 27 60
gcgcaccagc cacaccgagg cgtcatcgag gctgtctacc tgcgtactcc attctcagct 28 20
ggtaacgcca ccacataa                                     28 38

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&lt;210&gt; 106

&lt;211&gt; 945

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 30 Hexon

&lt;400&gt; 106

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
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Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20          25          30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
35          40          45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50          55          60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65          70          75          80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
85          90          95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
100         105         110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115         120         125
Ala Pro Asn Pro Ser Gln Trp Leu Glu Gln Ser Thr Thr Glu Gly Glu
130         135         140
Asp Asp Pro Thr Asn Thr Thr His Thr Phe Gly Ile Ala Ser Met Lys
145         150         155         160
Gly Glu Asn Ile Thr Lys Glu Gly Leu Gln Ile Gly Lys Glu Val Thr
165         170         175
Thr Thr Gly Asp Lys Pro Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu
180         185         190
Pro Gln Val Gly Glu Glu Thr Trp Thr Asp Thr Asp Gly Thr Asn Glu
195         200         205
Lys Phe Gly Gly Arg Thr Leu Lys Ser Ala Thr Asn Met Lys Pro Cys
210         215         220
Tyr Gly Ser Phe Ala Arg Pro Thr Asn Lys Gln Gly Gly Gln Ala Lys
225         230         235         240
Thr Arg Lys Val Ala Ala Val Asp Gly Gly Glu Glu Thr Glu Glu Pro
245         250         255
Asp Ile Asp Met Val Phe Tyr Asp Asp Arg Gly Ala Thr Glu Ala Met
260         265         270
Met Ala Pro Glu Val Val Leu Tyr Ala Glu Asn Val Asn Leu Glu Thr
275         280         285
Pro Asp Thr His Val Val Tyr Lys Pro Gly Thr Ser Asp Ile Asn Ser
290         295         300

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His	Glu	Asn	Leu	Gly	Gln	Gln	Ala	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile
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Gly	Phe	Arg	Asp	Asn	Phe	Val	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly
				325					330						335
Asn	Met	Gly	Val	Leu	Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val
				340					345				350		
Asp	Leu	Gln	Asp	Arg	Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp
		355					360					365			
Ser	Leu	Gly	Asp	Arg	Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val
370						375						380			
Asp	Ser	Tyr	Asp	Pro	Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Ile	Glu
385					390					395					400
Asp	Glu	Leu	Pro	Asn	Tyr	Cys	Phe	Pro	Leu	Asp	Gly	Ile	Gly	Pro	Gly
				405					410					415	
Lys	Thr	Tyr	Gln	Gly	Ile	Lys	Glu	Lys	Gln	Gly	Asp	Glu	Ala	Asn	Lys
			420					425					430		
Trp	Glu	Gln	Asp	Lys	Thr	Tyr	Ala	Thr	Ser	Asn	Glu	Ile	Ala	Ile	Gly
			435				440					445			
Asn	Asn	Leu	Ala	Met	Glu	Ile	Asn	Ile	Gln	Ala	Asn	Leu	Trp	Arg	Ser
					450		455				460				
Phe	Leu	Tyr	Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ala	Tyr	Lys	Tyr
465					470					475					480
Thr	Pro	Ala	Asn	Ile	Thr	Leu	Pro	Ala	Asn	Thr	Asn	Thr	Tyr	Glu	Tyr
				485					490					495	
Met	Asn	Gly	Arg	Val	Val	Ala	Pro	Ser	Leu	Val	Asp	Ser	Tyr	Ile	Asn
			500					505					510		
Ile	Gly	Ala	Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	Phe
		515					520					525			
Asn	His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly
	530					535					540				
Asn	Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe
545					550					555					560
Ala	Ile	Lys	Asn	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp
				565					570					575	
Asn	Phe	Arg	Lys	Asp	Val	Asn	Met	Val	Leu	Gln	Ser	Ser	Leu	Gly	Asn
			580					585					590		
Asp	Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn	Leu
		595				600						605			
Tyr	Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu
	610					615					620				
Ala	Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu
625					630					635					640
Ser	Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Ile
				645					650					655	
Pro	Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ser
			660					665					670		
Phe	Thr	Arg	Leu	Lys	Thr	Lys	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe
		675					680					685			
Asp	Pro	Tyr	Phe	Val	Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr
	690					695					700				
Phe	Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	Val	Ser	Ile	Met	Phe	Asp	Ser
705					710					715					720
Ser	Val	Ser	Trp	Pro	Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe
				725					730					735	



Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys  
 740 745 750  
 Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn  
 755 760 765  
 Ile Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Gly Tyr Lys Asp Arg Met  
 770 775 780  
 Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp  
 785 790 795 800  
 Glu Val Asn Tyr Lys Glu Tyr Gln Ala Val Thr Leu Ala Tyr Gln His  
 805 810 815  
 Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly  
 820 825 830  
 Glu Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Thr Thr Ala  
 835 840 845  
 Val Lys Ser Val Thr His Lys Lys Phe Leu Cys Asp Arg Thr Met Trp  
 850 855 860  
 Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp  
 865 870 875 880  
 Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ser His Ala Leu Asp Met  
 885 890 895  
 Thr Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Leu Leu  
 900 905 910  
 Phe Glu Val Phe Asp Val Val Arg Ala His Gln Pro His Arg Gly Val  
 915 920 925  
 Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr  
 930 935 940  
 Thr  
 945

&lt;210&gt; 107

&lt;211&gt; 2877

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 31 Hexon

&lt;400&gt; 107

atggcgaccc catcgatgat gccgcagtggt tcgtacatgc acatctcggg ccaggacgcc 60  
 tcggagtagc tgagccccgg gctgggtgcag ttcgcccgc g ccaccgagag ctacttcagc 120  
 ctgagtaaca agtttaggaa cccacgggtg gcgcccacgc acgatgtgac caccgaccgg 180  
 tctcagcgcc tgacgctgcg gttcattccc gtggaccgc g aggacaccgc gtactcgtac 240  
 aaggcgcggt tcaccctggc cgtggggcgac aaccgcgtgc tggacatggc ctccacctac 300  
 tttgacatcc gcgggggtgct ggaccggggc cccactttc a agccttactc tggcaccgcc 360  
 tacaactccc tggcccccaa gggcgctccc aactcctgc g agtgggagca attagaagaa 420  
 gcccaggccg ctgtggaaga cgaagaatta gaagatgaa g acgaggaacc acaggatgag 480  
 gcacctgtga aaaaaaccca tgtatacgct caggctccc c tttctggaga agaaattact 540  
 aaaaacgggt tgcaaatagg gtcagataac acagaagcc c agtctaagcc catatatgca 600  
 gatcctacat tccagcctga accccaaatc ggggaatcc c agtggaatga ggcagatgct 660  
 acagttgccc gcggtagagt gctaaagaaa tccactccc a tgaagccatg ctatggttcc 720  
 tatgcaagac ccacaaactc caatggaggt caaggtgtg c tgggtggctga tgataagggg 780  
 gttcttcaat ctaaagttga attgcaattt ttttcaaata ctactactct taatcagcgg 840  
 gagggtaacg atacaaaacc aaaagtgggtg ctgtatagc g aagatgtgca catggaaaact 900  
 ccagacaccc acatttctta caagcccaca aaaagcgat g acaattcaaa aatcatgctg 960  
 ggtcagcagt ccatgcccac cagacctaata tacatcggc t tcagagacaa ctttatcggc 1020  
 ctcatgtatt acaatagcac tggcaacatg ggagtgcct g caggtcaggc ctctcagttg 1080  
 aatgcagtggt tggacttgca agacagaaac acagaactgt cctaccagct cttgttgat 1140  
 tccatgggtg acagaaccag atacttttcc atgtggaat c aggcagtgga cagttatgac 1200

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ccagatgtca gaattattga aaatcatgga actgaagacg agctcccca a ctattgtttc 1260
cctctgggcg gcataggggt aactgacact taccaggcca ttaaaacca a tggcaatggg 1320
caagaaaacc caacctggga aaaagataca gagtttgcag accgcaatg a aataggggtg 1380
ggaaacaatt ttgctatgga gatcaacctc agtgccaacc tgtggagaa a cttcctgtac 1440
tccaacgtgg cgctgtacct accagacaag cttaagtaca acccctcca a tgtggacatc 1500
tctgacaacc ccaacaccta cgattacatg aacaagcgag tgggtggccc c ggggctgggtg 1560
gactgtctaca tcaacctggg cgcgcgctgg tcgctggact acatggaca a cgtcaacccc 1620
ttcaaccacc accgcaatgc gggcctgcgc taccgctcca tgctcctgg g caacgggcgc 1680
tatgtgcctt tccacatcca ggtgccccag aagttctttg ccatcaaga a cctcctcctc 1740
ctgccgggct cctacaccta cgagtgggaa ttcaggaagg atgtcaaca t ggtcctccag 1800
agctctctgg gtaacgatct cagggtggac ggggccagca tcaagttcg a gagcatctgc 1860
ctctacgcca cttcttccc catggcccac aacacggcct ccacgctcg a ggccatgctc 1920
aggaacgaca ccaacgacca gtcttcaat gactaccttt ccgccgcca a catgctctac 1980
cccatacccg ccaacgccac caacgtcccc atctccatcc cctcgcgca a ctgggcggcc 2040
ttccgcggtt gggccttcac ccgcctcaag accaaggaga cccctccc t gggctcggga 2100
ttcgacccct actacaccta ctcggtctct attccctacc tggacggca c cttctacctc 2160
aaccacactt tcaagaaggc ctcggtcacc ttcgactcct cggtcagct g gccgggcaac 2220
gaccgtctgc tcaccccaa cgagttcgag atcaagcgct cggtcgacg g ggaggctac 2280
aacgtggccc agtgcaacat gaccaaggac tggttcctgg tccagatgc t ggccaactac 2340
aacatcggtt accagggctt ctacatccca gagagctaca aggacagga t gtactccttc 2400
ttcaggaact tccagcccat gagccggcag gtggtggacc agaccaagt a caaggactac 2460
caggaggtgg gcatcatcca ccagcacaac aactcgggct tcgtgggct a cctcgcccc 2520
accatgcgcg agggacaggc ctaccccgcc aacttcccct acccgctca t aggcaagacc 2580
gcggtcgaca gcatcaccca gaaaaagttc ctctgcgacc gcaccctct g gcgcatcccc 2640
ttctccagca acttcatgtc catgggtgcg ctctcgacc tgggccagaa cttgctctac 2700
gccaaactccg ccacgcctt cgacatgacc ttcgaggtcg accccatgga cgagcccacc 2760
cttctctatg ttctgttcga agtctttgac gtggtccggg tccaccagc c gcaccgcggc 2820
gtcatcgaga ccgtgtacct gcgtacgccc ttctcgggcg gcaacgcca c cacctaa 2877

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&lt;210&gt; 108

&lt;211&gt; 958

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 31 Hexon

&lt;400&gt; 108

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Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser
1          5          10          15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20          25          30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
35          40          45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50          55          60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65          70          75          80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
85          90          95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
100          105          110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115          120          125
Ala Pro Asn Ser Cys Glu Trp Glu Gln Leu Glu Glu Ala Gln Ala Ala
130          135          140
Val Glu Asp Glu Glu Leu Glu Asp Glu Asp Glu Glu Pro Gln Asp Glu
145          150          155          160

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Ala	Pro	Val	Lys	Lys	Thr	His	Val	Tyr	Ala	Gln	Ala	Pro	Leu	Ser	Gly
				165					170					175	
Glu	Glu	Ile	Thr	Lys	Asn	Gly	Leu	Gln	Ile	Gly	Ser	Asp	Asn	Thr	Glu
			180					185						190	
Ala	Gln	Ser	Lys	Pro	Ile	Tyr	Ala	Asp	Pro	Thr	Phe	Gln	Pro	Glu	Pro
		195					200					205			
Gln	Ile	Gly	Glu	Ser	Gln	Trp	Asn	Glu	Ala	Asp	Ala	Thr	Val	Ala	Gly
	210					215						220			
Gly	Arg	Val	Leu	Lys	Lys	Ser	Thr	Pro	Met	Lys	Pro	Cys	Tyr	Gly	Ser
225				230						235					240
Tyr	Ala	Arg	Pro	Thr	Asn	Ser	Asn	Gly	Gly	Gln	Gly	Val	Leu	Val	Ala
				245				250						255	
Asp	Asp	Lys	Gly	Val	Leu	Gln	Ser	Lys	Val	Glu	Leu	Gln	Phe	Phe	Ser
			260					265					270		
Asn	Thr	Thr	Thr	Leu	Asn	Gln	Arg	Glu	Gly	Asn	Asp	Thr	Lys	Pro	Lys
		275					280					285			
Val	Val	Leu	Tyr	Ser	Glu	Asp	Val	His	Met	Glu	Thr	Pro	Asp	Thr	His
	290					295					300				
Ile	Ser	Tyr	Lys	Pro	Thr	Lys	Ser	Asp	Asp	Asn	Ser	Lys	Ile	Met	Leu
305					310					315					320
Gly	Gln	Gln	Ser	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp
				325					330					335	
Asn	Phe	Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val
			340					345					350		
Leu	Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp
		355					360					365			
Arg	Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Met	Gly	Asp
	370					375					380				
Arg	Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp
385					390					395					400
Pro	Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Thr	Glu	Asp	Glu	Leu	Pro
				405					410					415	
Asn	Tyr	Cys	Phe	Pro	Leu	Gly	Gly	Ile	Gly	Val	Thr	Asp	Thr	Tyr	Gln
			420					425					430		
Ala	Ile	Lys	Thr	Asn	Gly	Asn	Gly	Gln	Glu	Asn	Pro	Thr	Trp	Glu	Lys
		435					440					445			
Asp	Thr	Glu	Phe	Ala	Asp	Arg	Asn	Glu	Ile	Gly	Val	Gly	Asn	Asn	Phe
	450				455						460				
Ala	Met	Glu	Ile	Asn	Leu	Ser	Ala	Asn	Leu	Trp	Arg	Asn	Phe	Leu	Tyr
465					470					475					480
Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Lys	Leu	Lys	Tyr	Asn	Pro	Ser
				485					490					495	
Asn	Val	Asp	Ile	Ser	Asp	Asn	Pro	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Lys
		500						505					510		
Arg	Val	Val	Ala	Pro	Gly	Leu	Val	Asp	Cys	Tyr	Ile	Asn	Leu	Gly	Ala
		515					520					525			
Arg	Trp	Ser	Leu	Asp	Tyr	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His
	530					535					540				
Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg
545					550					555					560
Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys
				565					570					575	
Asn	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg
			580					585					590		

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Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
595 600 605
Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr Ala Thr
610 615 620
Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
625 630 635 640
Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
645 650 655
Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
660 665 670
Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe Thr Arg
675 680 685
Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
690 695 700
Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
705 710 715 720
Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser Val Ser
725 730 735
Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
740 745 750
Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr
755 760 765
Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr
770 775 780
Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr Ser Phe
785 790 795 800
Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln Thr Lys
805 810 815
Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn Asn Ser
820 825 830
Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln Ala Tyr
835 840 845
Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val Asp Ser
850 855 860
Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg Ile Pro
865 870 875 880
Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Ser Asp Leu Gly Gln
885 890 895
Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu
900 905 910
Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val
915 920 925
Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Thr
930 935 940
Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945 950 955

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&lt;210&gt; 109

&lt;211&gt; 2856

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 37 Hexon

&lt;400&gt; 109

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atggccaccc catcgatgct gccccagtgg gcatacatgc acatcgccgg acaggatgct 60
tcggagtacc tgagtccggg tctggtgcag ttcgcccgtg ccacagacac ctacttcaat 120

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ctggggaaca agtttaggaa cccaccgtg gccctaccc acgatgtgac cacCgaccgt 180
agccagcggc tgatgctgcg ctttgtgcc gttgatcggg aggacaatac ctaCtcttac 240
aaagtctcgt acacactggc tgtgggcgac aacagagtgc tggacatggc cagCaccttc 300
tttgacatca ggggggtgct tgacagaggt cccagtttca agccatactc tggCacagct 360
tacaattccc tggcgccctaa gggcgcgccc aatacatgcc agtggattgc caaGggggcg 420
cctgttaccg atcaagacaa tgaagaacag gaattaacag atgttactta cgcTtttggc 480
aatgctccag tacaagcaga agccaaaatt acaaaagatg gtctgccagt aggTttggaa 540
attacagaag atgaacaaaa gtcaatttat gcagacaaat tgtatcagcc agaGcccaa 600
attggcgatg aacaatggca tgacaccact ggcactaatg aacaatacgg cggCagagct 660
ctaaaaccgg ccaccaacat gaaaccatgt tatggctcat ttgccagacc cacaataaaa 720
aaaggcggtc aggctaaaac tagaaaaata gaaaaggaag agaattggagt taaaaccgta 780
actgaagaag ctgacattga tatggacttt tatgacttaa gatcacaag agcaaatttt 840
gatcctaaaa ttgttcttta ttctgaaaat gttaaatttg aaactccaga tacacatatt 900
gtgtataaac caggaacaga tgaaactagt tcctctgtta acttgggaca gcaGgcaatg 960
cccaacagac ccaactacat tggtttttag gacaacttca ttggacttat gttTtacaac 1020
agtaccggca acatgggctg gctggccggg caagcttctc agttaaagtc tgtGgttgac 1080
ttgcaggaca ggaacacaga actgtcctac cagctgctgc ttgactctct gggTgcacaga 1140
accagatact ttagcatgtg gaatcaggcc gtggatagct atgaccaga cgtGcgcat 1200
attgaaaacc acggtgtgga agacgaactt cctaactatt gttttccatt agatggagt 1260
ggaccaatta cgggcactta tcagggggtt gagcctgatg gaaacaatgg aaaCtggaag 1320
aaaaacacaa acataaatgg agcaaatgaa attggcaagg gaaataacta tgctatggaa 1380
attaatctac aagctaacct ctggagaagt ttctatatt ccaatgtggc tctGtattta 1440
ccagacggtt acaaatatac cccagccaat gttacactgc cagaaaacaa aaaCacctat 1500
ggctatataa acggacgagt agtatcccca tctttggtgg attcatacat caaCattgga 1560
gccagatggt ctttggatct tatggacaat gtaaaccat tcaatcacca ccGaatgca 1620
ggcctgcgtt accgtttccat gcttttagga aatggtcgt atgtgcctt ccaCaccgaa 1680
gtgcctcaga aaatctttgc tgtcaagaac ctgtgtctt tcccggctc ctaCacctat 1740
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agaactgatg gtgctagcat cagttttacc agcatcaatc tatatgtac cttTttcccc 1860
atggcccaca aactgcttc cacccttgaa gccatgctgc gcaatgacac caatgaccag 1920
tcatttaaatg actacctttc tgcagctaac atgctctacc ctattccagc caatgcaacc 1980
aacatcccca tttccattcc ctctcgcaat tgggcccgtc tcaggggctg gtcCttcacc 2040
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tctggttcta ttccctacct tgatggcacc ttctacctta accacacttt caagaaaggc 2160
tccatcatgt ttgactcctc agtcagctgg ccaggcaatg acaggcttct aactccaaat 2220
gagtttgaaa tcaaacgcac tgtggatggg gaagggtaca atgtggctca atgCaacatg 2280
accaaggact ggttcctggt tcaaatgctc gccaaactaca acattggcta ccaGgggctt 2340
tacatcccag aggggtacaa ggatcgcatg tactccttct tcagaaactt ccaGccccatg 2400
agtaggcagg tggttgatga gatcaactac aaggagtacc aagctgtcac actTgcttac 2460
cagcacaaca actctggctt tgtgggttac catgcacca ctctccgta gggTcaacca 2520
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gacatgactt ttgaggtgga tcccatggat gagcccacac tgctttatct tctTttcgaa 2760
gtcttcgacg tggtcagagt gcaccagcca caccgcggcg tcatcgagge cgtCtacctg 2820
cgcacaccgt tctcgccgg caacgccacc acataa 2856

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&lt;210&gt; 110

&lt;211&gt; 951

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 37 Hexon

&lt;400&gt; 110

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala

1

5

10

15

Gly	Gln	Asp	Ala	Ser	Glu	Tyr	Leu	Ser	Pro	Gly	Leu	Val	Gln	Phe	Ala		
			20					25					30				
Arg	Ala	Thr	Asp	Thr	Tyr	Phe	Asn	Leu	Gly	Asn	Lys	Phe	Arg	Asn	Pro		
		35					40					45					
Thr	Val	Ala	Pro	Thr	His	Asp	Val	Thr	Thr	Asp	Arg	Ser	Gln	Arg	Leu		
	50					55					60						
Met	Leu	Arg	Phe	Val	Pro	Val	Asp	Arg	Glu	Asp	Asn	Thr	Tyr	Ser	Tyr		
65					70					75					80		
Lys	Val	Arg	Tyr	Thr	Leu	Ala	Val	Gly	Asp	Asn	Arg	Val	Leu	Asp	Met		
				85					90					95			
Ala	Ser	Thr	Phe	Phe	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Pro	Ser		
			100					105					110				
Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly		
		115					120					125					
Ala	Pro	Asn	Thr	Cys	Gln	Trp	Ile	Ala	Lys	Gly	Ala	Pro	Val	Thr	Asp		
	130					135					140						
Gln	Asp	Asn	Glu	Glu	Gln	Glu	Leu	Thr	Asp	Val	Thr	Tyr	Ala	Phe	Gly		
145					150					155					160		
Asn	Ala	Pro	Val	Gln	Ala	Glu	Ala	Lys	Ile	Thr	Lys	Asp	Gly	Leu	Pro		
				165					170					175			
Val	Gly	Leu	Glu	Ile	Thr	Glu	Asp	Glu	Gln	Lys	Ser	Ile	Tyr	Ala	Asp		
			180					185					190				
Lys	Leu	Tyr	Gln	Pro	Glu	Pro	Gln	Ile	Gly	Asp	Glu	Gln	Trp	His	Asp		
	195						200					205					
Thr	Thr	Gly	Thr	Asn	Glu	Gln	Tyr	Gly	Gly	Arg	Ala	Leu	Lys	Pro	Ala		
	210					215					220						
Thr	Asn	Met	Lys	Pro	Cys	Tyr	Gly	Ser	Phe	Ala	Arg	Pro	Thr	Asn	Lys		
225					230				235						240		
Lys	Gly	Gly	Gln	Ala	Lys	Thr	Arg	Lys	Ile	Glu	Lys	Glu	Glu	Asn	Gly		
			245						250					255			
Val	Lys	Thr	Val	Thr	Glu	Glu	Ala	Asp	Ile	Asp	Met	Asp	Phe	Tyr	Asp		
			260					265					270				
Leu	Arg	Ser	Gln	Arg	Ala	Asn	Phe	Asp	Pro	Lys	Ile	Val	Leu	Tyr	Ser		
	275						280					285					
Glu	Asn	Val	Asn	Leu	Glu	Thr	Pro	Asp	Thr	His	Ile	Val	Tyr	Lys	Pro		
	290					295					300						
Gly	Thr	Asp	Glu	Thr	Ser	Ser	Ser	Val	Asn	Leu	Gly	Gln	Gln	Ala	Met		
305					310					315					320		
Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe	Ile	Gly	Leu		
				325					330					335			
Met	Phe	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala	Gly	Gln	Ala		
			340					345					350				
Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn	Thr	Glu	Leu		
	355						360					365					
Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly	Asp	Arg	Thr	Arg	Tyr	Phe		
	370					375					380						
Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	Val	Arg	Ile		
385					390					395					400		
Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu	Pro	Asn	Tyr	Cys	Phe	Pro		
			405						410					415			
Leu	Asp	Gly	Val	Gly	Pro	Ile	Thr	Gly	Thr	Tyr	Gln	Gly	Val	Glu	Pro		
			420					425					430				
Asp	Gly	Asn	Asn	Gly	Asn	Trp	Lys	Lys	Asn	Thr	Asn	Ile	Asn	Gly	Ala		
		435					440					445					

Asn	Glu	Ile	Gly	Lys	Gly	Asn	Asn	Tyr	Ala	Met	Glu	Ile	Asn	Leu	Gln
450						455					460				
Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr	Ser	Asn	Val	Ala	Leu	Tyr	Leu
465					470					475					480
Pro	Asp	Gly	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	Val	Thr	Leu	Pro	Glu	Asn
				485					490						495
Lys	Asn	Thr	Tyr	Gly	Tyr	Ile	Asn	Gly	Arg	Val	Val	Ser	Pro	Ser	Leu
			500					505					510		
Val	Asp	Ser	Tyr	Ile	Asn	Ile	Gly	Ala	Arg	Trp	Ser	Leu	Asp	Leu	Met
		515					520					525			
Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr
		530				535					540				
Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln
545					550					555					560
Val	Pro	Gln	Lys	Ile	Phe	Ala	Val	Lys	Asn	Leu	Leu	Leu	Leu	Pro	Gly
			565						570						575
Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn	Met	Val	Leu
			580					585					590		
Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	Ser
		595				600						605			
Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn
	610					615					620				
Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln
625					630					635					640
Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro
			645						650						655
Ala	Asn	Ala	Thr	Asn	Ile	Pro	Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala
			660					665						670	
Ala	Phe	Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	Lys	Thr	Lys	Glu	Thr	Pro
		675					680					685			
Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Phe	Val	Tyr	Ser	Gly	Ser	Ile
	690					695					700				
Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	Val
705					710					715					720
Ser	Ile	Met	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn	Asp	Arg	Leu
			725						730						735
Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	Thr	Val	Asp	Gly	Glu	Gly
			740					745					750		
Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe	Leu	Val	Gln
	755						760					765			
Met	Leu	Ala	Asn	Tyr	Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr	Ile	Pro	Glu
	770					775					780				
Gly	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe	Gln	Pro	Met
785					790					795					800
Ser	Arg	Gln	Val	Val	Asp	Glu	Ile	Asn	Tyr	Lys	Glu	Tyr	Gln	Ala	Val
			805						810						815
Thr	Leu	Ala	Tyr	Gln	His	Asn	Asn	Ser	Gly	Phe	Val	Gly	Tyr	His	Ala
			820					825					830		
Pro	Thr	Leu	Arg	Gln	Gly	Gln	Pro	Tyr	Pro	Ala	Asn	Tyr	Pro	Tyr	Pro
		835					840					845			
Leu	Ile	Gly	Thr	Thr	Ala	Val	Thr	Ser	Val	Thr	Gln	Lys	Lys	Phe	Leu
	850					855					860				
Cys	Asp	Arg	Thr	Met	Trp	Arg	Ile	Pro	Phe	Ser	Ser	Asn	Phe	Met	Ser
865					870					875					880

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<210> 111
<211> 2817
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 38 Hexon
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ttccgcaact tccaacccat gagccgccag gtgggtggacg aggtcaacta caaggactac 2400
caggccgtca ccctggccta ccagcacaac aactcgggct tcgtcggcta cctcgcgccc 2460
accatgcgcc agggccagcc ctaccccgcc aactaccctt acccggtcat cggcaagagc 2520
gccgtcacca gcgtcaccca gaaaaagttc ctctgcgaca ggggtcatgtg gcgcatcccc 2580
ttctccagca acttcatgtc catggggcgcg ctcaccgacc tcggccagaa catgctctat 2640
gccaaactccg cccacgcgct agacatgaat ttcgaagtcg accccatgga tgagtccacc 2700
cttctctatg ttgtcttcga agtcttcgac gtcgtccgag tgcaccagcc ccaccgcggc 2760
gtcatcgagg ccgtctacct gcgcaccccc ttctcggccg gtaacgccac cacctaa 2817

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&lt;210&gt; 112

&lt;211&gt; 938

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 38 Hexon

&lt;400&gt; 112

```

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1           5           10           15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
          20           25           30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
          35           40           45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
          50           55           60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65           70           75           80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
          85           90           95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
          100          105          110
Phe Lys-Pro Tyr Ser Gly Thr Ala Tyr Asn Ala Leu Ala Pro Lys Ala
          115          120          125
Ala Pro Asn Pro Ser Gln Trp Glu Glu Thr Thr Thr Gly Thr Asp Gly
          130          135          140
Asn Ala Ala Thr Thr Thr Thr His Ser Phe Gly Leu Ala Ala Met Lys
145          150          155          160
Gly Asp Asn Ile Thr Ser Asp Gly Leu Gln Ile Gly Thr Asp Ala Thr
          165          170          175
Ser Gly Glu Glu Lys Pro Ile Tyr Ala Asp Lys Leu Tyr Gln Pro Glu
          180          185          190
Pro Gln Ile Gly Glu Glu Ser Trp Thr Asp Thr Asp Gly Thr Asn Glu
          195          200          205
Lys Phe Gly Gly Arg Val Leu Lys Lys Asp Thr Ser Met Lys Pro Cys
          210          215          220
Tyr Gly Ser Phe Ala Lys Pro Thr Asn Asn Lys Gly Gly Gln Ala Lys
225          230          235          240
Gln Lys Ala Thr Glu Gly Thr Ala Val Glu Tyr Asp Val Asp Met Asn
          245          250          255
Phe Phe Asp Gly Arg Asp Ala Ala Ala Asn Phe Thr Pro Glu Val Val
          260          265          270
Leu Tyr Ala Glu Asn Val Asp Leu Glu Thr Pro Asp Thr His Ile Val
          275          280          285
Tyr Lys Pro Gly Thr Ser Asp Val Ser Ser His Val Asn Leu Gly Gln
          290          295          300

```

Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe  
 305 310 315 320  
 Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala  
 325 330 335  
 Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn  
 340 345 350  
 Thr Glu Leu Ser Tyr Gln Leu Leu Asp Ser Leu Gly Asp Arg Thr  
 355 360 365  
 Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp  
 370 375 380  
 Val Arg Ile Ile Glu Asn His Gly Ile Glu Asp Glu Leu Pro Asn Tyr  
 385 390 395 400  
 Cys Phe Pro Ile Asp Ala Val Gly Ile Thr Arg Thr Tyr Gln Gly Ile  
 405 410 415  
 Lys Thr Gln Asn Gly Gln Thr Thr Thr Trp Glu Lys Asp Thr Ser Val  
 420 425 430  
 Ser Thr Ala Asn Glu Ile Gly Ile Gly Asn Asn Leu Ala Met Glu Ile  
 435 440 445  
 Asn Ile Gln Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala  
 450 455 460  
 Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Val Thr Leu  
 465 470 475 480  
 Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala  
 485 490 495  
 Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu  
 500 505 510  
 Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly  
 515 520 525  
 Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe  
 530 535 540  
 His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu  
 545 550 555 560  
 Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn  
 565 570 575  
 Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala  
 580 585 590  
 Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met  
 595 600 605  
 Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr  
 610 615 620  
 Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr  
 625 630 635 640  
 Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg  
 645 650 655  
 Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys  
 660 665 670  
 Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser  
 675 680 685  
 Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe  
 690 695 700  
 Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn  
 705 710 715 720  
 Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp  
 725 730 735

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<210> 113
<211> 2781
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 44 Hexon
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tacacgccgg ccaacgtcac cctgcccacc aacaccaaca cctacgatta catgaacggg 1440
agagtgggtgc ctccctcgct ggtggacgcc tacatcaaca tcggggcgcg ctggtcgctg 1500
gaccccatgg acaacgtgaa ccccttcaac caccaccgca acgcgggggt gcgctaccgc 1560
tccatgctcc tgggcaacgg gcgcttcgtg cccttccaca tccaggtgcc ccagaaattt 1620
ttcgccatca agagcctcct gctcctgcca gggtcctaca cctacgagtg gaacttccgc 1680
aaggacgtca acatgatcct gcagagctcc ctgggcaacg acctgcgcac ggacggggcc 1740
tccatctcct tcaccagtat caacctctac gccaccttct tcccatggc gcacaacacg 1800
gcctccacgc tcgaggccat gctgcgcaac gacaccaacg accagtcctt caacgactac 1860
ctctcgggcg ccaacatgct ctaccccatc ccggccaacg ccaccaacgt gcccatctcc 1920
atccctcgc gcaactgggc cgcttccgc gggtggtcct tcacgcgcct caagaccaag 1980
gagacgccct cgctgggctc cgggttcgac ccctacttcg tctactcggt ctccatcccc 2040
tacctcgacg gcaccttcta cctcaaccac accttcaaga aggtctccat caccttcgac 2100
tcctccgtca gctggcccgg caacgaccgc ctctgacgc ccaacgagtt cgaaatcaag 2160
cgcaccgtcg acggagaggg gtacaacgtg gccagtgca acatgaccaa ggactgggtc 2220
ctggtccaga tgctggccca ctacaacatc ggctaccagg gcttctacgt gcccaggggc 2280
tacaaggacc gcatgtactc cttcttcgc aacttccagc ccatgagccg ccaggtgggtg 2340
gacgaggtca actacaagga ctaccaggcc gtcacctgg cctaccagca gaacaactcg 2400
ggcttcgtcg gctacctcgc gccaccatg gccaggggc agccctacc cgccaactac 2460
ccgtaccgc tcatcgga gagcgccgtc accagcgta cccagaaaaa gttcctctgc 2520
gacaggttca tgtggcgcat ccccttctcc agcaacttca tgtccatggg cgcgctcacc 2580
gacctcgcc agaacatgct ctatgccaac tccgccacg cgctagacat gaatttcgaa 2640
gtcgacccca tggatgagtc cacccttctc tatgttgtct tcgaagtctt cgacgtcgtc 2700
cgagtgcacc agccccaccg cggcgctcgc gagggcgtct acctgcgcac ccccttctcg 2760
gccggtaacg ccaccaccta a 2781

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&lt;210&gt; 114

&lt;211&gt; 926

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 44 Hexon

&lt;400&gt; 114

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1      5      10
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20     25     30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
35     40     45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50     55     60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65     70     75     80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
85     90     95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
100    105    110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115    120    125
Ala Pro Asn Pro Ser Gln Trp Glu Gln Thr Glu Thr Asn Val Asn Lys
130    135    140
Thr His Thr Phe Gly Met Ala Ala Met Lys Gly Glu Ala Ile Asp Lys
145    150    155    160
Asn Gly Leu Gln Ile Gly Thr Asp Ala Ala Asp Gln Asp Lys Pro Ile
165    170    175

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Tyr	Ala	Asp	Lys	Thr	Phe	Gln	Pro	Glu	Pro	Gln	Val	Gly	Glu	Glu	Asp		
			180					185					190				
Trp	Ile	Asp	Lys	Ala	Asp	Phe	Tyr	Gly	Gly	Arg	Ala	Leu	Lys	Lys	Asp		
		195					200					205					
Thr	Lys	Met	Lys	Pro	Cys	Tyr	Gly	Ser	Phe	Ala	Lys	Pro	Thr	Asn	Val		
	210					215					220						
Lys	Gly	Gly	Gln	Ala	Thr	Pro	Arg	Thr	Lys	Ala	Asp	Gly	Thr	Thr	Glu		
225					230					235					240		
Pro	Asp	Ile	Asp	Met	Asn	Phe	Phe	Asp	Pro	Thr	Thr	Ile	Asn	Thr	Pro		
			245					250					255				
Asp	Val	Val	Leu	Tyr	Ala	Glu	Asn	Val	Asp	Leu	Gln	Thr	Pro	Asp	Thr		
			260					265					270				
His	Ile	Val	Tyr	Lys	Ala	Gly	Thr	Ser	Asp	Asp	Ser	Ser	Glu	Val	Asn		
	275						280					285					
Leu	Ala	Gln	Gln	Ala	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg		
	290					295				300							
Asp	Asn	Phe	Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly		
305					310					315					320		
Val	Leu	Ala	Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln		
				325					330					335			
Asp	Arg	Asn	Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly		
			340					345					350				
Asp	Arg	Thr	Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr		
	355						360					365					
Asp	Pro	Asp	Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu		
	370					375					380						
Pro	Asn	Tyr	Cys	Phe	Pro	Leu	Asp	Gly	Val	Gly	Thr	Asn	Thr	Ala	Tyr		
385					390					395					400		
Gln	Gly	Val	Lys	Val	Lys	Thr	Thr	Asn	Gly	Asn	Asp	Thr	Trp	Glu	Lys		
				405					410					415			
Asp	Glu	Thr	Val	Tyr	Glu	Phe	Asn	Gln	Ile	Gly	Lys	Gly	Asp	Ile	Tyr		
			420					425					430				
Ala	Met	Glu	Ile	Asn	Ile	Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr		
	435						440					445					
Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr	Pro	Ala		
	450					455					460						
Asn	Val	Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Gly		
465					470					475					480		
Arg	Val	Val	Pro	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Ile	Asn	Ile	Gly	Ala		
				485					490					495			
Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His		
			500					505					510				
Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg		
	515						520					525					
Phe	Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys		
	530					535					540						
Ser	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg		
545					550					555					560		
Lys	Asp	Val	Asn	Met	Ile	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg		
				565					570					575			
Thr	Asp	Gly	Ala	Ser	Ile	Ser	Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr		
			580					585					590				
Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu		
		595					600					605					

Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala  
 610 615 620  
 Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser  
 625 630 635 640  
 Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg  
 645 650 655  
 Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr  
 660 665 670  
 Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu  
 675 680 685  
 Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser  
 690 695 700  
 Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys  
 705 710 715 720  
 Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr  
 725 730 735  
 Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr  
 740 745 750  
 Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe  
 755 760 765  
 Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn  
 770 775 780  
 Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser  
 785 790 795 800  
 Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr  
 805 810 815  
 Pro-Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser  
 820 825 830  
 Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro  
 835 840 845  
 Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln  
 850 855 860  
 Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu  
 865 870 875 880  
 Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val  
 885 890 895  
 Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala  
 900 905 910  
 Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 915 920 925

&lt;210&gt; 115

&lt;211&gt; 2877

&lt;212&gt; DNA

&lt;213&gt; Chimpanzee Adenovirus- ChAd 63 Hexon

&lt;400&gt; 115

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 ctgagtcagg gtctggtgca gttcgccccgc gccacagaca cctacttcag tctggggaac 180  
 aagtttagga accccacggt ggcgcccacg cacgatgtga ccaccgaccg cagccagcgg 240  
 ctgacgctgc gcttcgtgcc cgtggaccgc gaggacaaca cctactcgta caaagtgcgc 300  
 tacacgctgg ccgtgggcga caaccgcgtg ctggacatgg ccagcaccta ctttgacatc 360  
 cgcggcgtgc tggatcgggg cccagcttc aaaccctact ccggcaccgc ctacaacagc 420  
 ctagctccca agggagcgcc caacacctca cagtggaagg attccgacag caaatgcat 480

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acttttggag ttgctgccat gccgggtgtt gttggtaaaa aaatagaagc cgatgggtctg 540
cctattggaa tagattcatc ctctggaact gacaccataa tttatgctga taaaactttc 600
caaccagagc cacagggttg aagtgcagct tgggtcgaca ccaatgggtgc agaggaaaaa 660
tatggaggta gagctcttaa ggacactaca aacatgaagc cctgctacgg ttcttttgcc 720
aggcctacca acaaagaagg tggacaggct aacataaaag attctgaaac tgccagcact 780
actcctaact atgatataga tttggcattc tttgacagca aaaatattgc agctaactac 840
gatccagata ttgtaatgta cacagaaaat gttgagttgc aaactccaga tactcatatt 900
gtgtttaagc caggaacttc agatgaaagt tcagaagcca atttgggccca gcaggccatg 960
cccaacagac ccaactacat cgggttcaga gacaacttta tcgggctcat gtactacaac 1020
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ttgcaggaca gaaacaccga actgtcctac cagctcttgc ttgactctct gggtgacaga 1140
accaggtatt tcagtatgtg gaatcaggcg gtggacagct atgacccga tgtgcgcatt 1200
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&lt;210&gt; 116

&lt;211&gt; 941

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 63 Hexon

&lt;400&gt; 116

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Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1           5           10           15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20           25           30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
35           40           45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50           55           60

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Thr	Leu	Arg	Phe	Val	Pro	Val	Asp	Arg	Glu	Asp	Asn	Thr	Tyr	Ser	Tyr	65	70	75	80
Lys	Val	Arg	Tyr	Thr	Leu	Ala	Val	Gly	Asp	Asn	Arg	Val	Leu	Asp	Met	85	90		95
Ala	Ser	Thr	Tyr	Phe	Asp	Ile	Arg	Gly	Val	Leu	Asp	Arg	Gly	Pro	Ser	100	105		110
Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly	115	120		125
Ala	Pro	Asn	Thr	Ser	Gln	Trp	Lys	Asp	Ser	Asp	Ser	Lys	Met	His	Thr	130	135		140
Phe	Gly	Val	Ala	Ala	Met	Pro	Gly	Val	Val	Gly	Lys	Lys	Ile	Glu	Ala	145	150		155
Asp	Gly	Leu	Pro	Ile	Gly	Ile	Asp	Ser	Ser	Ser	Gly	Thr	Asp	Thr	Ile	165	170		175
Ile	Tyr	Ala	Asp	Lys	Thr	Phe	Gln	Pro	Glu	Pro	Gln	Val	Gly	Ser	Asp	180	185		190
Ser	Trp	Val	Asp	Thr	Asn	Gly	Ala	Glu	Glu	Lys	Tyr	Gly	Gly	Arg	Ala	195	200		205
Leu	Lys	Asp	Thr	Thr	Asn	Met	Lys	Pro	Cys	Tyr	Gly	Ser	Phe	Ala	Arg	210	215		220
Pro	Thr	Asn	Lys	Glu	Gly	Gly	Gln	Ala	Asn	Ile	Lys	Asp	Ser	Glu	Thr	225	230		235
Ala	Ser	Thr	Thr	Pro	Asn	Tyr	Asp	Ile	Asp	Leu	Ala	Phe	Phe	Asp	Ser	245	250		255
Lys	Asn	Ile	Ala	Ala	Asn	Tyr	Asp	Pro	Asp	Ile	Val	Met	Tyr	Thr	Glu	260	265		270
Asn	Val	Glu	Leu	Gln	Thr	Pro	Asp	Thr	His	Ile	Val	Phe	Lys	Pro	Gly	275	280		285
Thr	Ser	Asp	Glu	Ser	Ser	Glu	Ala	Asn	Leu	Gly	Gln	Gln	Ala	Met	Pro	290	295		300
Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe	Ile	Gly	Leu	Met	305	310		315
Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala	Gly	Gln	Ala	Ser	325	330		335
Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn	Thr	Glu	Leu	Ser	340	345		350
Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly	Asp	Arg	Thr	Arg	Tyr	Phe	Ser	355	360		365
Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	Val	Arg	Ile	Ile	370	375		380
Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu	Pro	Asn	Tyr	Cys	Phe	Pro	Leu	385	390		395
Asn	Gly	Val	Gly	Phe	Thr	Asp	Thr	Tyr	Gln	Gly	Val	Lys	Val	Lys	Thr	405	410		415
Asp	Thr	Ala	Ala	Thr	Gly	Thr	Asn	Gly	Thr	Gln	Trp	Asp	Lys	Asp	Asp	420	425		430
Thr	Thr	Val	Ser	Thr	Ala	Asn	Glu	Ile	His	Ser	Gly	Asn	Pro	Phe	Ala	435	440		445
Met	Glu	Ile	Asn	Ile	Gln	Ala	Asn	Leu	Trp	Arg	Asn	Phe	Leu	Tyr	Ala	450	455		460
Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	465	470		475
Ile	Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Gly	Arg	485	490		495



Val	Val	Ala	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Ile	Asn	Ile	Gly	Ala	Arg	500	505	510
Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	515	520	525
Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	530	535	540
Val	Pro	Phe	His	Ile	Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys	Ser	545	550	555
Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	565	570	575
Asp	Val	Asn	Met	Ile	Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Thr	580	585	590
Asp	Gly	Ala	Ser	Ile	Ala	Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	595	600	605
Phe	Pro	Met	Ala	His	Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	610	615	620
Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	625	630	635
Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	645	650	655
Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	660	665	670
Lys	Thr	Arg	Glu	Thr	Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Phe	675	680	685
Val	Tyr	Ser	Gly	Ser	Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	690	695	700
His	Thr	Phe	Lys	Lys	Val	Ser	Ile	Thr	Phe	Asp	Ser	Ser	Val	Ser	Trp	705	710	715
Pro	Gly	Asn	Asp	Arg	Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	725	730	735
Thr	Val	Asp	Gly	Glu	Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	740	745	750
Asp	Trp	Phe	Leu	Val	Gln	Met	Leu	Ala	His	Tyr	Asn	Ile	Gly	Tyr	Gln	755	760	765
Gly	Phe	Tyr	Val	Pro	Glu	Gly	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	770	775	780
Arg	Asn	Phe	Gln	Pro	Met	Ser	Arg	Gln	Val	Val	Asp	Glu	Val	Asn	Tyr	785	790	795
Lys	Asp	Tyr	Gln	Ala	Val	Thr	Leu	Ala	Tyr	Gln	His	Asn	Asn	Ser	Gly	805	810	815
Phe	Val	Gly	Tyr	Leu	Ala	Pro	Thr	Met	Arg	Gln	Gly	Gln	Pro	Tyr	Pro	820	825	830
Ala	Asn	Tyr	Pro	Tyr	Pro	Leu	Ile	Gly	Lys	Ser	Ala	Val	Ala	Ser	Val	835	840	845
Thr	Gln	Lys	Lys	Phe	Leu	Cys	Asp	Arg	Val	Met	Trp	Arg	Ile	Pro	Phe	850	855	860
Ser	Ser	Asn	Phe	Met	Ser	Met	Gly	Ala	Leu	Thr	Asp	Leu	Gly	Gln	Asn	865	870	875
Met	Leu	Tyr	Ala	Asn	Ser	Ala	His	Ala	Leu	Asp	Met	Asn	Phe	Glu	Val	885	890	895
Asp	Pro	Met	Asp	Glu	Ser	Thr	Leu	Leu	Tyr	Val	Val	Phe	Glu	Val	Phe	900	905	910
Asp	Val	Val	Arg	Val	His	Gln	Pro	His	Arg	Gly	Val	Ile	Glu	Ala	Val	915	920	925

Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 930 935 940

<210> 117

<211> 2811

<212> DNA

<213> Chimpanzee Adenovirus- ChAd 82 Hexon

<400> 117

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ctggggaaca agtttaggaa cccacgggtg gcgcccacgc acgatgtgac caccgaccgc 180
agccagcggc tgacgtgctg cttcgtgccc gtggaccgcg aggacaacac ctactcgtac 240
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2811

<213> Chimpanzee Adenovirus- ChAd 82 Hexon

- 175 -

Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	370	375	380
Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu	Pro	Asn	Tyr	385	390	395
Cys	Phe	Pro	Leu	Asp	Gly	Ala	Gly	Thr	Asn	Ala	Val	Tyr	Arg	Gly	Val	405	410	415
Lys	Ala	Lys	Asp	Asn	Gly	Asn	Trp	Glu	Gln	Asp	Thr	Gly	Val	Ser	Ser	420	425	430
Ile	Asn	Gln	Ile	Cys	Lys	Gly	Asn	Ile	Tyr	Ala	Met	Glu	Ile	Asn	Ile	435	440	445
Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr	Ser	Asn	Val	Ala	Leu	Tyr	450	455	460
Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	Ile	Thr	Leu	Pro	Thr	465	470	475
Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Gly	Arg	Val	Val	Pro	Pro	Ser	485	490	495
Leu	Val	Asp	Ala	Tyr	Ile	Asn	Ile	Gly	Ala	Arg	Trp	Ser	Leu	Asp	Pro	500	505	510
Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn	Ala	Gly	Leu	Arg	515	520	525
Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	530	535	540
Gln	Val	Pro	Gln	Lys	Phe	Phe	Ala	Ile	Lys	Ser	Leu	Leu	Leu	Leu	Pro	545	550	555
Gly	Ser	Tyr	Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn	Met	Ile	565	570	575
Leu	Gln	Ser	Ser	Leu	Gly	Asn	Asp	Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	580	585	590
Ser	Phe	Thr	Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met	Ala	His	595	600	605
Asn	Thr	Ala	Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	610	615	620
Gln	Ser	Phe	Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	625	630	635
Pro	Ala	Asn	Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	645	650	655
Ala	Ala	Phe	Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	Lys	Thr	Lys	Glu	Thr	660	665	670
Pro	Ser	Leu	Gly	Ser	Gly	Phe	Asp	Pro	Tyr	Phe	Val	Tyr	Ser	Gly	Ser	675	680	685
Ile	Pro	Tyr	Leu	Asp	Gly	Thr	Phe	Tyr	Leu	Asn	His	Thr	Phe	Lys	Lys	690	695	700
Val	Ser	Ile	Thr	Phe	Asp	Ser	Ser	Val	Ser	Trp	Pro	Gly	Asn	Asp	Arg	705	710	715
Leu	Leu	Thr	Pro	Asn	Glu	Phe	Glu	Ile	Lys	Arg	Thr	Val	Asp	Gly	Glu	725	730	735
Gly	Tyr	Asn	Val	Ala	Gln	Cys	Asn	Met	Thr	Lys	Asp	Trp	Phe	Leu	Val	740	745	750
Gln	Met	Leu	Ala	His	Tyr	Asn	Ile	Gly	Tyr	Gln	Gly	Phe	Tyr	Val	Pro	755	760	765
Glu	Gly	Tyr	Lys	Asp	Arg	Met	Tyr	Ser	Phe	Phe	Arg	Asn	Phe	Gln	Pro	770	775	780
Met	Ser	Arg	Gln	Val	Val	Asp	Glu	Val	Asn	Tyr	Lys	Asp	Tyr	Gln	Ala	785	790	795
																		800

Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu  
805 810 815  
Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr  
820 825 830  
Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr Gln Lys Lys Phe  
835 840 845  
Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met  
850 855 860  
Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn  
865 870 875 880  
Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu  
885 890 895  
Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val  
900 905 910  
His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro  
915 920 925  
Phe Ser Ala Gly Asn Ala Thr Thr  
930 935

&lt;210&gt; 119

&lt;211&gt; 933

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV23 Pan5 Hexon

&lt;400&gt; 119

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Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
20 25 30  
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro  
35 40 45  
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
50 55 60  
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
65 70 75 80  
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
85 90 95  
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
100 105 110  
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
115 120 125  
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Asp Gly Asp Thr Gly  
130 135 140  
Thr Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser  
145 150 155 160  
Ile Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Thr Asp Asp Gln Pro  
165 170 175  
Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala  
180 185 190  
Glu Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala  
195 200 205  
Leu Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys  
210 215 220  
Pro Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly  
225 230 235 240

Gly	Thr	Lys	Glu	Tyr	Asp	Ile	Asp	Met	Ala	Phe	Phe	Asp	Asn	Arg	Ser	
				245					250					255		
Ala	Ala	Ala	Ala	Gly	Leu	Ala	Pro	Glu	Ile	Val	Leu	Tyr	Thr	Glu	Asn	
			260					265						270		
Val	Asp	Leu	Glu	Thr	Pro	Asp	Thr	His	Ile	Val	Tyr	Lys	Ala	Gly	Thr	
	275						280					285				
Asp	Asp	Ser	Ser	Ser	Ser	Ile	Asn	Leu	Gly	Gln	Gln	Ser	Met	Pro	Asn	
	290					295					300					
Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe	Ile	Gly	Leu	Met	Tyr	
305					310					315					320	
Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala	Gly	Gln	Ala	Ser	Gln	
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Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn	Thr	Glu	Leu	Ser	Tyr	
			340					345					350			
Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly	Asp	Arg	Thr	Arg	Tyr	Phe	Ser	Met	
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Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp	Val	Arg	Ile	Ile	Glu	
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Ala	Val	Gly	Arg	Thr	Asp	Thr	Tyr	Gln	Gly	Ile	Lys	Ala	Asn	Gly	Ala	
				405					410					415		
Asp	Gln	Thr	Thr	Trp	Thr	Lys	Asp	Asp	Thr	Val	Asn	Asp	Ala	Asn	Glu	
			420					425					430			
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Leu	Trp	Arg	Asn	Phe	Leu	Tyr	Ala	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	
	450					455					460					
Ser	Tyr	Lys	Tyr	Thr	Pro	Ala	Asn	Ile	Thr	Leu	Pro	Thr	Asn	Thr	Asn	
465					470					475					480	
Thr	Tyr	Asp	Tyr	Met	Asn	Gly	Arg	Val	Val	Ala	Pro	Ser	Leu	Val	Asp	
				485					490					495		
Ala	Tyr	Ile	Asn	Ile	Gly	Ala	Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	
			500					505					510			
Val	Asn	Pro	Phe	Asn	His	His	Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	
	515						520					525				
Met	Leu	Leu	Gly	Asn	Gly	Arg	Tyr	Val	Pro	Phe	His	Ile	Gln	Val	Pro	
	530				535						540					
Gln	Lys	Phe	Phe	Ala	Ile	Lys	Ser	Leu	Leu	Leu	Leu	Pro	Gly	Ser	Tyr	
545					550					555					560	
Thr	Tyr	Glu	Trp	Asn	Phe	Arg	Lys	Asp	Val	Asn	Met	Ile	Leu	Gln	Ser	
				565					570					575		
Ser	Leu	Gly	Asn	Asp	Leu	Arg	Thr	Asp	Gly	Ala	Ser	Ile	Ala	Phe	Thr	
			580					585					590			
Ser	Ile	Asn	Leu	Tyr	Ala	Thr	Phe	Phe	Pro	Met	Ala	His	Asn	Thr	Ala	
	595					600						605				
Ser	Thr	Leu	Glu	Ala	Met	Leu	Arg	Asn	Asp	Thr	Asn	Asp	Gln	Ser	Phe	
	610					615					620					
Asn	Asp	Tyr	Leu	Ser	Ala	Ala	Asn	Met	Leu	Tyr	Pro	Ile	Pro	Ala	Asn	
625					630					635					640	
Ala	Thr	Asn	Val	Pro	Ile	Ser	Ile	Pro	Ser	Arg	Asn	Trp	Ala	Ala	Phe	
				645					650					655		
Arg	Gly	Trp	Ser	Phe	Thr	Arg	Leu	Lys	Thr	Arg	Glu	Thr	Pro	Ser	Leu	
			660					665					670			

Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr  
           675                                  680                                  685  
 Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile  
           690                                  695                                  700  
 Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr  
   705                                  710                                  715                                  720  
 Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn  
                                   725                                  730                                  735  
 Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu  
                                   740                                  745                                  750  
 Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr  
                                   755                                  760                                  765  
 Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg  
           770                                  775                                  780  
 Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu  
   785                                  790                                  795                                  800  
 Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr  
                                   805                                  810                                  815  
 Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile  
                                   820                                  825                                  830  
 Gly Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp  
           835                                  840                                  845  
 Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly  
   850                                  855                                  860  
 Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His  
   865                                  870                                  875                                  880  
 Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu  
                                   885                                  890                                  895  
 Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro  
                                   900                                  905                                  910  
 His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala  
           915                                  920                                  925  
 Gly Asn Ala Thr Thr  
           930

&lt;210&gt; 120

&lt;211&gt; 942

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV32 Pan6 Hexon

&lt;400&gt; 120

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala  
   1                                  5                                  10                                  15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
           20                                  25                                  30  
 Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro  
           35                                  40                                  45  
 Thr Val Ala Pro Thr His Asn Val Thr Thr Asp Arg Ser Gln Arg Leu  
   50                                  55                                  60  
 Thr Val Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
   65                                  70                                  75                                  80  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
           85                                  90                                  95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
           100                                  105                                  110

Phe	Lys	Pro	Tyr	Ser	Gly	Thr	Ala	Tyr	Asn	Ser	Leu	Ala	Pro	Lys	Gly		
		115					120					125					
Ala	Pro	Asn	Ser	Ser	Gln	Trp	Glu	Gln	Ala	Lys	Thr	Gly	Asn	Gly	Gly		
	130					135						140					
Thr	Met	Glu	Thr	His	Thr	Tyr	Gly	Val	Ala	Pro	Met	Gly	Gly	Glu	Asn		
145					150					155					160		
Ile	Thr	Lys	Asp	Gly	Leu	Gln	Ile	Gly	Thr	Asp	Val	Thr	Ala	Asn	Gln		
				165					170						175		
Asn	Lys	Pro	Ile	Tyr	Ala	Asp	Lys	Thr	Phe	Gln	Pro	Glu	Pro	Gln	Val		
			180					185						190			
Gly	Glu	Glu	Asn	Trp	Gln	Glu	Thr	Glu	Asn	Phe	Tyr	Gly	Gly	Arg	Ala		
		195					200					205					
Leu	Lys	Lys	Asp	Thr	Asn	Met	Lys	Pro	Cys	Tyr	Gly	Ser	Tyr	Ala	Arg		
	210					215					220						
Pro	Thr	Asn	Glu	Lys	Gly	Gly	Gln	Ala	Lys	Leu	Lys	Val	Gly	Asp	Asp		
225					230					235					240		
Gly	Val	Pro	Thr	Lys	Glu	Phe	Asp	Ile	Asp	Leu	Ala	Phe	Phe	Asp	Thr		
				245					250					255			
Pro	Gly	Gly	Thr	Val	Asn	Gly	Gln	Asp	Glu	Tyr	Lys	Ala	Asp	Ile	Val		
			260					265						270			
Met	Tyr	Thr	Glu	Asn	Thr	Tyr	Leu	Glu	Thr	Pro	Asp	Thr	His	Val	Val		
		275					280					285					
Tyr	Lys	Pro	Gly	Lys	Asp	Asp	Ala	Ser	Ser	Glu	Ile	Asn	Leu	Val	Gln		
	290					295					300						
Gln	Ser	Met	Pro	Asn	Arg	Pro	Asn	Tyr	Ile	Gly	Phe	Arg	Asp	Asn	Phe		
305					310					315					320		
Ile	Gly	Leu	Met	Tyr	Tyr	Asn	Ser	Thr	Gly	Asn	Met	Gly	Val	Leu	Ala		
				325					330					335			
Gly	Gln	Ala	Ser	Gln	Leu	Asn	Ala	Val	Val	Asp	Leu	Gln	Asp	Arg	Asn		
			340					345					350				
Thr	Glu	Leu	Ser	Tyr	Gln	Leu	Leu	Leu	Asp	Ser	Leu	Gly	Asp	Arg	Thr		
		355					360					365					
Arg	Tyr	Phe	Ser	Met	Trp	Asn	Gln	Ala	Val	Asp	Ser	Tyr	Asp	Pro	Asp		
	370					375					380						
Val	Arg	Ile	Ile	Glu	Asn	His	Gly	Val	Glu	Asp	Glu	Leu	Pro	Asn	Tyr		
385					390					395					400		
Cys	Phe	Pro	Leu	Asp	Gly	Ser	Gly	Thr	Asn	Ala	Ala	Tyr	Gln	Gly	Val		
				405					410					415			
Lys	Val	Lys	Asp	Gly	Gln	Asp	Gly	Asp	Val	Glu	Ser	Glu	Trp	Glu	Asn		
			420					425					430				
Asp	Asp	Thr	Val	Ala	Ala	Arg	Asn	Gln	Leu	Cys	Lys	Gly	Asn	Ile	Phe		
		435					440					445					
Ala	Met	Glu	Ile	Asn	Leu	Gln	Ala	Asn	Leu	Trp	Arg	Ser	Phe	Leu	Tyr		
	450					455						460					
Ser	Asn	Val	Ala	Leu	Tyr	Leu	Pro	Asp	Ser	Tyr	Lys	Tyr	Thr	Pro	Thr		
465					470					475					480		
Asn	Val	Thr	Leu	Pro	Thr	Asn	Thr	Asn	Thr	Tyr	Asp	Tyr	Met	Asn	Gly		
				485					490					495			
Arg	Val	Thr	Pro	Pro	Ser	Leu	Val	Asp	Ala	Tyr	Leu	Asn	Ile	Gly	Ala		
			500					505					510				
Arg	Trp	Ser	Leu	Asp	Pro	Met	Asp	Asn	Val	Asn	Pro	Phe	Asn	His	His		
	515						520					525					
Arg	Asn	Ala	Gly	Leu	Arg	Tyr	Arg	Ser	Met	Leu	Leu	Gly	Asn	Gly	Arg		
	530					535					540						



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Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys
545                    550                    555                    560
Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg
                    565                    570                    575
Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
                    580                    585                    590
Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn Leu Tyr Ala Thr
                    595                    600                    605
Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
610                    615                    620
Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
625                    630                    635                    640
Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
                    645                    650                    655
Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg
660                    665                    670
Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
675                    680                    685
Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
690                    695                    700
Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser
705                    710                    715                    720
Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
725                    730                    735
Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr
740                    745                    750
Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr
755                    760                    765
Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe
770                    775                    780
Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn
785                    790                    795                    800
Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser
805                    810                    815
Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr
820                    825                    830
Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser
835                    840                    845
Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro
850                    855                    860
Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln
865                    870                    875                    880
Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu
885                    890                    895
Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val
900                    905                    910
Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala
915                    920                    925
Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
930                    935                    940

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&lt;210&gt; 121

&lt;211&gt; 932

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV33 Pan7 Hexon

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<400> 121
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1      5      10      15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20      25      30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
35      40      45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50      55      60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65      70      75      80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
85      90      95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
100     105     110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115     120     125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Gly Asp Thr Asp Thr
130     135     140
Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser Ile
145     150     155     160
Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Ser Asp Gly Gln Ala Ile
165     170     175
Tyr Ala Asp Glu Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala Glu
180     185     190
Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala Leu
195     200     205
Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro
210     215     220
Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly Gly
225     230     235     240
Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser Ala
245     250     255
Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn Val
260     265     270
Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp
275     280     285
Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg
290     295     300
Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr
305     310     315     320
Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu
325     330     335
Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln
340     345     350
Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp
355     360     365
Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn
370     375     380
His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp Ala
385     390     395     400
Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Asp Asn
405     410     415

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Gln Thr Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu Leu  
 420 425 430  
 Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn Leu  
 435 440 445  
 Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp Ser  
 450 455 460  
 Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn Thr  
 465 470 475 480  
 Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ala  
 485 490 495  
 Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val  
 500 505 510  
 Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met  
 515 520 525  
 Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln  
 530 535 540  
 Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr  
 545 550 555 560  
 Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser  
 565 570 575  
 Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser  
 580 585 590  
 Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser  
 595 600 605  
 Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn  
 610 615 620  
 Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala  
 625 630 635 640  
 Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg  
 645 650 655  
 Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly  
 660 665 670  
 Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu  
 675 680 685  
 Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr  
 690 695 700  
 Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro  
 705 710 715 720  
 Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val  
 725 730 735  
 Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala  
 740 745 750  
 His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys  
 755 760 765  
 Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln  
 770 775 780  
 Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala  
 785 790 795 800  
 Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met  
 805 810 815  
 Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly  
 820 825 830  
 Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg  
 835 840 845

Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala  
 850 855 860  
 Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala  
 865 870 875 880  
 Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu  
 885 890 895  
 Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His  
 900 905 910  
 Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly  
 915 920 925  
 Asn Ala Thr Thr  
 930

<210> 122

<211> 960

<212> PRT

<213> Chimpanzee Adenovirus- ChAd 3 Hexon

<400> 122

Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr  
 65 70 75 80  
 Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Ser Cys Glu Trp Glu Gln Glu Glu Thr Gln Ala Val Glu  
 130 135 140  
 Glu Ala Ala Glu Glu Glu Glu Asp Ala Asp Gly Gln Ala Glu Glu  
 145 150 155 160  
 Glu Gln Ala Ala Thr Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu  
 165 170 175  
 Ser Gly Glu Lys Ile Ser Lys Asp Gly Leu Gln Ile Gly Thr Asp Ala  
 180 185 190  
 Thr Ala Thr Glu Gln Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro  
 195 200 205  
 Glu Pro Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val  
 210 215 220  
 Ala Gly Gly Arg Val Leu Lys Lys Ser Thr Pro Met Lys Pro Cys Tyr  
 225 230 235 240  
 Gly Ser Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu  
 245 250 255  
 Thr Ala Asn Ala Gln Gly Gln Leu Glu Ser Gln Val Glu Met Gln Phe  
 260 265 270  
 Phe Ser Thr Ser Glu Asn Ala Arg Asn Glu Ala Asn Asn Ile Gln Pro  
 275 280 285

Lys Leu Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr  
 290 295 300  
 His Leu Ser Tyr Lys Pro Ala Lys Ser Asp Asp Asn Ser Lys Ile Met  
 305 310 315 320  
 Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg  
 325 330 335  
 Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly  
 340 345 350  
 Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln  
 355 360 365  
 Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly  
 370 375 380  
 Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr  
 385 390 395 400  
 Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu  
 405 410 415  
 Pro Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr  
 420 425 430  
 Gln Ala Val Lys Thr Asn Asn Gly Asn Asn Gly Gly Gln Val Thr Trp  
 435 440 445  
 Thr Lys Asp Glu Thr Phe Ala Asp Arg Asn Glu Ile Gly Val Gly Asn  
 450 455 460  
 Asn Phe Ala Met Glu Ile Asn Leu Ser Ala Asn Leu Trp Arg Asn Phe  
 465 470 475 480  
 Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn  
 485 490 495  
 Pro Ser Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met  
 500 505 510  
 Asn Lys Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu  
 515 520 525  
 Gly Ala Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn  
 530 535 540  
 His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn  
 545 550 555 560  
 Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala  
 565 570 575  
 Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn  
 580 585 590  
 Phe Arg Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp  
 595 600 605  
 Leu Arg Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr  
 610 615 620  
 Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala  
 625 630 635 640  
 Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser  
 645 650 655  
 Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro  
 660 665 670  
 Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe  
 675 680 685  
 Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp  
 690 695 700  
 Pro Tyr Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe  
 705 710 715 720

Tyr Leu Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser  
 725 730 735  
 Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu  
 740 745 750  
 Ile Lys Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn  
 755 760 765  
 Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile  
 770 775 780  
 Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr  
 785 790 795 800  
 Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln  
 805 810 815  
 Thr Lys Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn  
 820 825 830  
 Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln  
 835 840 845  
 Ala Tyr Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val  
 850 855 860  
 Asp Ser Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg  
 865 870 875 880  
 Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Ser Asp Leu  
 885 890 895  
 Gly Gln Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr  
 900 905 910  
 Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe  
 915 920 925  
 Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile  
 930 935 940  
 Glu Thr Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 945 950 955 960

&lt;210&gt; 123

&lt;211&gt; 937

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- ChAd 6 Hexon

&lt;400&gt; 123

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
 65 70 75 80  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Thr Ser Gln Trp Ile Thr Lys Asp Asn Gly Thr Asp Lys  
 130 135 140

Thr Tyr Ser Phe Gly Asn Ala Pro Val Arg Gly Leu Asp Ile Thr Glu  
 145 150 155 160  
 Glu Gly Leu Gln Ile Gly Pro Asp Glu Ser Gly Gly Glu Ser Lys Lys  
 165 170 175  
 Ile Phe Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Leu Gly Asp Glu  
 180 185 190  
 Glu Trp His Asp Thr Ile Gly Ala Glu Asp Lys Tyr Gly Gly Arg Ala  
 195 200 205  
 Leu Lys Pro Ala Thr Asn Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys  
 210 215 220  
 Pro Thr Asn Ala Lys Gly Gly Gln Ala Lys Ser Arg Thr Lys Asp Asp  
 225 230 235 240  
 Gly Thr Thr Glu Pro Asp Ile Asp Met Ala Phe Phe Asp Asp Arg Ser  
 245 250 255  
 Gln Gln Ala Ser Phe Ser Pro Glu Leu Val Leu Tyr Thr Glu Asn Val  
 260 265 270  
 Asp Leu Asp Thr Pro Asp Thr His Ile Ile Tyr Lys Pro Gly Thr Asp  
 275 280 285  
 Glu Thr Ser Ser Ser Phe Asn Leu Gly Gln Gln Ser Met Pro Asn Arg  
 290 295 300  
 Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr  
 305 310 315 320  
 Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu  
 325 330 335  
 Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln  
 340 345 350  
 Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp  
 355 360 365  
 Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn  
 370 375 380  
 His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asn Gly  
 385 390 395 400  
 Val Gly Phe Thr Asp Thr Phe Gln Gly Ile Lys Val Lys Thr Thr Asn  
 405 410 415  
 Asn Gly Thr Ala Asn Ala Thr Glu Trp Glu Ser Asp Thr Ser Val Asn  
 420 425 430  
 Asn Ala Asn Glu Ile Ala Lys Gly Asn Pro Phe Ala Met Glu Ile Asn  
 435 440 445  
 Ile Gln Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu  
 450 455 460  
 Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro  
 465 470 475 480  
 Ala Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro  
 485 490 495  
 Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp  
 500 505 510  
 Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu  
 515 520 525  
 Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His  
 530 535 540  
 Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu  
 545 550 555 560  
 Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met  
 565 570 575

Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser  
 580 585 590  
 Ile Ala Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala  
 595 600 605  
 His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn  
 610 615 620  
 Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro  
 625 630 635 640  
 Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn  
 645 650 655  
 Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu  
 660 665 670  
 Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly  
 675 680 685  
 Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys  
 690 695 700  
 Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp  
 705 710 715 720  
 Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly  
 725 730 735  
 Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu  
 740 745 750  
 Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val  
 755 760 765  
 Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln  
 770 775 780  
 Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln  
 785 790 795 800  
 Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr  
 805 810 815  
 Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro  
 820 825 830  
 Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys  
 835 840 845  
 Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe  
 850 855 860  
 Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala  
 865 870 875 880  
 Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp  
 885 890 895  
 Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg  
 900 905 910  
 Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr  
 915 920 925  
 Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 930 935

&lt;210&gt; 124

&lt;211&gt; 956

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- C1 Hexon

&lt;400&gt; 124

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala  
 1 5 10 15



Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
 65 70 75 80  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Ser Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Thr Ser Gln Trp Leu Asp Lys Gly Val Thr Thr Thr Asp  
 130 135 140  
 Asn Asn Thr Glu Asn Gly Asp Glu Glu Asp Glu Val Ala Glu Glu Gly  
 145 150 155 160  
 Glu Glu Glu Lys Gln Ala Thr Tyr Thr Phe Gly Asn Ala Pro Val Lys  
 165 170 175  
 Ala Glu Ala Glu Ile Thr Lys Glu Gly Leu Pro Ile Gly Leu Glu Val  
 180 185 190  
 Pro Ser Glu Gly Asp Pro Lys Pro Ile Tyr Ala Asp Lys Leu Tyr Gln  
 195 200 205  
 Pro Glu Pro Gln Val Gly Glu Glu Ser Trp Thr Asp Thr Asp Gly Thr  
 210 215 220  
 Asp Glu Lys Tyr Gly Gly Arg Ala Leu Lys Pro Glu Thr Lys Met Lys  
 225 230 235 240  
 Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn Val Lys Gly Gly Gln  
 245 250 255  
 Ala Lys Val Lys Lys Val Glu Glu Gly Lys Val Glu Tyr Asp Ile Asp  
 260 265 270  
 Met Asn Phe Phe Asp Leu Arg Ser Gln Lys Thr Gly Leu Lys Pro Lys  
 275 280 285  
 Ile Val Met Tyr Ala Glu Asn Val Asp Leu Glu Thr Pro Asp Thr His  
 290 295 300  
 Val Val Tyr Lys Pro Gly Ala Ser Asp Ala Ser Ser His Ala Asn Leu  
 305 310 315 320  
 Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp  
 325 330 335  
 Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val  
 340 345 350  
 Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp  
 355 360 365  
 Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp  
 370 375 380  
 Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp  
 385 390 395 400  
 Pro Asp Val Arg Val Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro  
 405 410 415  
 Asn Tyr Cys Phe Pro Leu Asp Gly Val Gly Pro Arg Thr Asp Ser Tyr  
 420 425 430  
 Lys Gly Ile Glu Thr Asn Gly Asp Glu Asn Thr Thr Trp Lys Asp Leu  
 435 440 445

Asp Pro Asn Gly Ile Ser Glu Leu Ala Lys Gly Asn Pro Phe Ala Met  
 450 455 460  
 Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn  
 465 470 475 480  
 Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Thr Asn Val  
 485 490 495  
 Thr Leu Pro Glu Asn Lys Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val  
 500 505 510  
 Val Pro Pro Ser Leu Val Asp Thr Tyr Val Asn Ile Gly Ala Arg Trp  
 515 520 525  
 Ser Leu Asp Ala Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn  
 530 535 540  
 Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val  
 545 550 555 560  
 Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Val Lys Asn Leu  
 565 570 575  
 Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp  
 580 585 590  
 Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Val Asp  
 595 600 605  
 Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe  
 610 615 620  
 Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn  
 625 630 635 640  
 Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met  
 645 650 655  
 Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro  
 660 665 670  
 Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys  
 675 680 685  
 Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val  
 690 695 700  
 Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His  
 705 710 715 720  
 Thr Phe Lys Lys Val Ser Ile Met Phe Asp Ser Ser Val Ser Trp Pro  
 725 730 735  
 Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr  
 740 745 750  
 Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp  
 755 760 765  
 Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly  
 770 775 780  
 Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg  
 785 790 795 800  
 Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Ile Asn Tyr Lys  
 805 810 815  
 Asp Tyr Lys Ala Val Ala Val Pro Tyr Gln His Asn Asn Ser Gly Phe  
 820 825 830  
 Val Gly Tyr Met Ala Pro Thr Met Arg Gln Gly Gln Ala Tyr Pro Ala  
 835 840 845  
 Asn Tyr Pro Tyr Pro Leu Ile Gly Thr Thr Ala Val Thr Ser Val Thr  
 850 855 860  
 Gln Lys Lys Phe Leu Cys Asp Arg Thr Met Trp Arg Ile Pro Phe Ser  
 865 870 875 880

Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Leu  
 885 890 895  
 Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp  
 900 905 910  
 Pro Met Asp Glu Pro Thr Leu Leu Tyr Leu Leu Phe Glu Val Phe Asp  
 915 920 925  
 Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr  
 930 935 940  
 Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr  
 945 950 955

&lt;210&gt; 125

&lt;211&gt; 933

&lt;212&gt; PRT

&lt;213&gt; Chimpanzee Adenovirus- CV68 Hexon

&lt;400&gt; 125

Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala  
 1 5 10 15  
 Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala  
 20 25 30  
 Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro  
 35 40 45  
 Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu  
 50 55 60  
 Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr  
 65 70 75 80  
 Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met  
 85 90 95  
 Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser  
 100 105 110  
 Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly  
 115 120 125  
 Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Asp Gly Glu Thr Ala  
 130 135 140  
 Thr Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Asn  
 145 150 155 160  
 Ile Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Thr Asp Asp Gln Pro  
 165 170 175  
 Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala  
 180 185 190  
 Glu Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala  
 195 200 205  
 Leu Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys  
 210 215 220  
 Pro Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Gly Thr Gly  
 225 230 235 240  
 Thr Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser  
 245 250 255  
 Ala Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn  
 260 265 270  
 Val Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr  
 275 280 285  
 Asp Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln Ala Met Pro Asn  
 290 295 300

Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr  
 305 310 315 320  
 Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln  
 325 330 335  
 Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr  
 340 345 350  
 Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met  
 355 360 365  
 Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu  
 370 375 380  
 Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp  
 385 390 395 400  
 Ala Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Thr  
 405 410 415  
 Asp Gln Thr Thr Trp Thr Lys Asp Asp Ser Val Asn Asp Ala Asn Glu  
 420 425 430  
 Ile Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn  
 435 440 445  
 Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp  
 450 455 460  
 Ser Tyr Lys Tyr Thr Pro Ala Asn Val Thr Leu Pro Thr Asn Thr Asn  
 465 470 475 480  
 Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp  
 485 490 495  
 Ser Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn  
 500 505 510  
 Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser  
 515 520 525  
 Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro  
 530 535 540  
 Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Pro Gly Ser Tyr  
 545 550 555 560  
 Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser  
 565 570 575  
 Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ser Phe Thr  
 580 585 590  
 Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala  
 595 600 605  
 Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe  
 610 615 620  
 Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn  
 625 630 635 640  
 Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe  
 645 650 655  
 Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu  
 660 665 670  
 Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr  
 675 680 685  
 Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile  
 690 695 700  
 Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr  
 705 710 715 720  
 Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn  
 725 730 735

[illegible]